

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: October 24, 2004, 11:03:18 ; Search time 137 Seconds

(without alignments)
1885.717 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

Sequence: 1 MLAVPASRNSQSDTVDQGY.....SFVGLSFARSGDWAECEFA 449

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2353	99.8	467	1	PHYA ASPNG
2	2324	98.6	467	2	Q679Z6
3	2324	98.6	467	2	AAR08366
4	2313	98.1	467	2	Q9U0Z7
5	2309	97.9	467	1	PHYA ASPAW
6	2279	96.6	448	2	Q8U255
7	2278	96.6	448	2	Q6J336
8	2278	96.6	448	2	AAT12504
9	2278	96.6	467	2	Q93838
10	2273	96.4	448	2	Q6GYA8
11	2268	96.2	467	2	Q9HEQ0
12	2265	96.1	467	2	Q6R519
13	2265	96.1	467	2	AAS00648
14	1617.5	68.6	465	1	PHYA ASPFU
15	1610	68.3	466	2	Q9C1T1
16	1605.5	68.1	442	2	Q8WZJ5
17	1534	65.1	463	1	PHYB EMENI
18	1520	64.5	466	2	Q00100
19	1501.5	63.7	466	2	Q00096
20	1493	63.3	466	1	PHYA ASPTE
21	1475	62.6	461	2	Q6VNE9
22	1475	62.6	461	2	AAL55406
23	1177	49.9	596	2	Q7S9V5
24	1135	48.1	487	1	PHYA THIEH
25	765.5	32.5	443	2	Q96VF5
26	752.5	31.9	439	2	Q96VH9
27	739.5	31.4	453	2	Q96V70
28	739	31.3	442	2	Q96VK9
29	732	31.0	442	2	Q96VK8
30	438	18.6	610	2	Q7SSH2
31	396	16.8	464	2	Q6BUR8

RESULT 1

PHYA ASPNG

ID PHYA ASPNG STANDARD; PRT; 467 AA.

AC P34752;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE 3-phytase A precursor (EC 3.1.3.8) (Myo-inositol-hexakisphosphate 3-

phosphohydrolase A) (3 phytase A) (Myo-inositol hexakisphosphate

phosphohydrolase A).

DE Name=PHYA;

OS Aspergillus niger.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

OX NCBI_TaxID=5061;

RN [1]

SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=NRRL 3135 / Van Tieghem / Ficum;

RX MEDLINE=93252284; PubMed=8387447;

RA van Hartingsveldt W., van Zeijl C.M.J., Harteveld G.M., Gouka R.J.,

RA Suykerbuyk M.E.G., Luiten R.G.M., van Paridon P.A., Selden G.C.M.,

RA Veenstra A.E., van Gorcom R.F.W., van den Hondel C.A.M.J.J.;

RT "Cloning, characterization and overexpression of the phytase-encoding

gene (phyA) of Aspergillus niger.";

RL Gene 127:87-94(1993).

RL [2]

SEQUENCE FROM N.A.

RP Mullaney E.J.;

RT "Sequence of the Aspergillus niger (ficum) phytase gene.";

RL Submitted (JUN-1992) to the EMBL/GenBank/DBSJ databases.

RL [3]

SEQUENCE OF 24-464.

RC STRAIN=NRRL 3135 / Van Tieghem / Ficum;

RX MEDLINE=93249451; PubMed=8387289;

RA Ullah A.H.J., Dischinger H.C. Jr.;

RT "Aspergillus ficum phytase: complete primary structure elucidation by

chemical sequencing.";

RL Biochem. Biophys. Res. Commun. 192:747-753(1993).

RL [4]

SEQUENCE OF 71-93.

RC STRAIN=NRRL 3135 / Van Tieghem / Ficum;

RX MEDLINE=91298982; PubMed=1648914;

RA Ullah A.H.J., Cummins B.J., Dischinger H.C. Jr.;

RT "Cyclohexanediol modification of arginine at the active site of

Aspergillus ficum phytase.";

RL Biochem. Biophys. Res. Commun. 178:45-53(1991).

RL [5]

CHARACTERIZATION, AND PARTIAL SEQUENCE.

RC STRAIN=NRRL 3135 / Van Tieghem / Ficum;

RX MEDLINE=89160685; PubMed=2852807;

RA Ullah A.H.J.;

RT "Aspergillus ficum phytase: partial primary structure, substrate

selectivity, and kinetic characterization.";

RL Prep. Biochem. 18:459-471(1988).

RL


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QY 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
DB 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGFSASAWTPFASRLYVEMMQCAEQEPLRVLVNDRVVPPLHGCVPD 421
DB 380 PLSTTTVENITQTDGFSASAWTPFASRLYVEMMQCAEQEPLRVLVNDRVVPPLHGCVPD 439
QY 422 ALGRCTRDSFVRGLSFARSGGDWAECEFA 449
DB 440 ALGRCTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 2
Q6T9Z6 PRELIMINARY; PRT; 467 AA.
ID Q6T9Z6
AC Q6T9Z6;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Phytase.
GN Name-phyA;
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]_TaxID=5061;
RP SEQUENCE FROM N.A.
RC STRAIN=N14*;
RA Peng Y.Y., Zhou Z.Y., Ma L.P.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY426977; AAR08366.1; -.
DR InterPro; IPR000560; HisAc_phosphatase.
DR Pfam; PF00328; Acid_phosphatase; 1.
DR PROSITE; PS00616; HIS ACID PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS ACID PHOSPHAT_2; 1.
SQ SEQUENCE 467 AA; 51142 MW; 2EAECD38865E94EF CRC64;

Query Match 98.6%; Score 2324; DB 2; Length 467;
Best Local Similarity 98.0%; Pred. No. 6.2e-165;
Matches 439; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQGYQCFSSETSHLWGQYAPFPFSLANESVISPEVPAGCRVTFAQVL 61
DB 20 LAVPASRNQSTCDTVDQGYQCFSSETSHLWGQYAPFPFSLANESVISPEVPAGCRVTFAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEIQQNATTFDGKYAFLKTYNYSGLGADDLTPFGEOELVNS 121
DB 80 SRHGARYPTDSKGGKYSALIEIQQNATTFDGKYAFLKTYNYSGLGADDLTPFGEOELVNS 139
QY 122 GIKFYQRYESLNTNIVPFRSSGSRVIAAGKFFIEGQSTKLDKDPRAQPGSSPKIDVV 181
DB 140 GIKFYQRYESLNTNIVPFRSSGSRVIAAGKFFIEGQSTKLDKDPRAQPGSSPKIDVV 199
QY 182 ISEASSNNLDPGCTVTFEDSELADTVANFTATFVPSIRQLENDLSGVLTITTEVTY 241
DB 200 ISEASSNNLDPGCTVTFEDSELADTVANFTATFVPSIRQLENDLSGVLTITTEVTY 259
QY 242 LDMCSEFDTISTNTVDTKLSPFCDLFTHEWINYDYLQSLKKYGHGAGNPLGPTQGVGY 301
DB 260 LDMCSEFDTISTNTVDTKLSPFCDLFTHEWINYDYLQSLKKYGHGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
DB 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGFSASAWTPFASRLYVEMMQCAEQEPLRVLVNDRVVPPLHGCVPD 421
DB 380 PLSTTTVENITQTDGFSASAWTPFASRLYVEMMQCAEQEPLRVLVNDRVVPPLHGCVPD 439
QY 422 ALGRCTRDSFVRGLSFARSGGDWAECEFA 449
DB 440 ALGRCTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 4
Q9UUZ7 PRELIMINARY; PRT; 467 AA.
ID Q9UUZ7
AC Q9UUZ7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 26, Last annotation update)
DE Myo-inositol hexaphosphate phosphohydrolyase precursor (EC 3.1.3.8).
OS Aspergillus niger.

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DB 440 ALGRCTRDSFVKGLSFARSGGDWAECEFA 467

RESULT 3
AAR08366 PRELIMINARY; PRT; 467 AA.
ID AAR08366
AC AAR08366;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE Phytase.
GN PHYA.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]_TaxID=5061;
RP SEQUENCE FROM N.A.
RC STRAIN=N14*;
RA Peng Y.Y., Zhou Z.Y., Ma L.P.;
RL "Cloning and characterization of phytase gene of Aspergillus niger N14*";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY426977; AAR08366.1; -.
DR EMBL; AY426977; AAR08366.1; -.
SQ SEQUENCE 467 AA; 51142 MW; 2EAECD38865E94EF CRC64;

Query Match 98.6%; Score 2324; DB 2; Length 467;
Best Local Similarity 98.0%; Pred. No. 6.2e-165;
Matches 439; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQGYQCFSSETSHLWGQYAPFPFSLANESVISPEVPAGCRVTFAQVL 61
DB 20 LAVPASRNQSTCDTVDQGYQCFSSETSHLWGQYAPFPFSLANESVISPEVPAGCRVTFAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEIQQNATTFDGKYAFLKTYNYSGLGADDLTPFGEOELVNS 121
DB 80 SRHGARYPTDSKGGKYSALIEIQQNATTFDGKYAFLKTYNYSGLGADDLTPFGEOELVNS 139
QY 122 GIKFYQRYESLNTNIVPFRSSGSRVIAAGKFFIEGQSTKLDKDPRAQPGSSPKIDVV 181
DB 140 GIKFYQRYESLNTNIVPFRSSGSRVIAAGKFFIEGQSTKLDKDPRAQPGSSPKIDVV 199
QY 182 ISEASSNNLDPGCTVTFEDSELADTVANFTATFVPSIRQLENDLSGVLTITTEVTY 241
DB 200 ISEASSNNLDPGCTVTFEDSELADTVANFTATFVPSIRQLENDLSGVLTITTEVTY 259
QY 242 LDMCSEFDTISTNTVDTKLSPFCDLFTHEWINYDYLQSLKKYGHGAGNPLGPTQGVGY 301
DB 260 LDMCSEFDTISTNTVDTKLSPFCDLFTHEWINYDYLQSLKKYGHGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
DB 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGFSASAWTPFASRLYVEMMQCAEQEPLRVLVNDRVVPPLHGCVPD 421
DB 380 PLSTTTVENITQTDGFSASAWTPFASRLYVEMMQCAEQEPLRVLVNDRVVPPLHGCVPD 439
QY 422 ALGRCTRDSFVRGLSFARSGGDWAECEFA 449
DB 440 ALGRCTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 4
Q9UUZ7 PRELIMINARY; PRT; 467 AA.
ID Q9UUZ7
AC Q9UUZ7;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 26, Last annotation update)
DE Myo-inositol hexaphosphate phosphohydrolyase precursor (EC 3.1.3.8).
OS Aspergillus niger.

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OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCB1_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RA Hongning W., Qi W., Jing X.;
RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF218813; AAF25481.1; -
DR HSP; P34752; 1IHP.
DR GO; GO:0003933; F:acid phosphatase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
DR InterPro; IPR000560; HisAc phspase.
DR Pfam; PF00328; Acid phosphat A; 1.
DR PROSITE; PS00616; HIS ACID PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS ACID PHOSPHAT_2; 1.
KW Hydrolase; Lyase; Signal.
FT SIGNAL 1 19 Potential.
SQ SEQUENCE 467 AA; 51029 MW; F4300A8F165BEP92 CRC64;

Query Match 98.1%; Score 2313; DB 2; Length 467;
Best Local Similarity 97.5%; Pred. No. 4.1e-164;
Matches 43; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 2 LAVPASRNSQSCDTVDQGYQCFSTSLWGQYAPFFSLANESVISPVPAGCRVTFQAQVL 61
DB 20 LAVPASRNSQSCDTVDQGYQCFSTSLWGQYAPFFSLANESVISPVPAGCRVTFQAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEEIQONATTPDGKVAFLKTYNSLGADDLTPFGQELVNS 121
DB 80 SRHGARYPTDSKGGKYSALIEEIQONATTPDGKVAFLKTYNSLGADDLTPFGQELVNS 139
QY 122 GIKFYQRYESLTRNIPFIRSSGSSRVASGKFIQGFQSTKLDPRAQCGQSSPKIDVV 181
DB 140 GIKFYQRYESLTRNIPFIRSSGSSRVASGKFIQGFQSTKLDPRAQCGQSSPKIDVV 199
QY 182 GIKFYQRYESLTRNIPFIRSSGSSRVASGKFIQGFQSTKLDPRAQCGQSSPKIDVV 241
DB 200 ISEASSNNLTDPGTCVFEDSELADTVEANFTATFVPSIRQRLNDSGLVTLTDTVTY 259
QY 242 LMDWCSFDTTSTVTDVTKLSPFCDLFDHDEWINYDIQSLKKYGHGAGNPLGTCQGVY 301
DB 260 LMDWCSFDTTSTVTDVTKLSPFCDLFDHDEWINYDIQSLKKYGHGAGNPLGTCQGVY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATPLNLTADFSHDNGIISILFALGLYNGTK 361
DB 320 ANELIARLTHSPVHDDTSSNHTLDSNATPLNLTADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTQDGFSSAWTVPPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCVD 421
DB 380 PLSTTTVENITQTQDGFSSAWTVPPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCVD 439
QY 422 ALGRCRTDSVRLGSLFARSQGDWAECPA 449
DB 440 ALGRCRTDSVRLGSLFARSQGDWAECPA 467

RESULT 5
PHYA ASPAW
ID PHYA ASPAW STANDARD; PRT; 467 AA.
AC P34753;
DT 01-FEB-1994 (Rel. 28, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 3-phytase A precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate 3-phosphohydrolase A).
DE Name=PHYA; Synonyms=PHY;
OS Aspergillus awamori.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCB1_TaxID=105351;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=ALK0243;
RA MEDLINE=94040796; PubMed=8224894;
RA Piddington C.S., Houston C.S., Paloheimo M.T., Cantrell M.A.,
RA Miettinen-Oinonen A., Nevalainen H., Rambosck J.A.;
RA "The cloning and sequencing of the genes encoding phytase (phy) and pH
RT 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
RT awamori".
RL Gene 133:55-62(1993).
CC -!- FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate
CC from phytate.
CC -!- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)O = 1D-
CC myo-inositol 1,2,4,5,6-pentakisphosphate + phosphate.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the histidine acid phosphatase family.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L02421; AAA16898.1; -.
DR PIR; JN0889; JN0889.
DR HSP; P34752; 1IHP.
DR InterPro; IPR000560; HisAc_phspase.
DR Pfam; PF00328; Acid phosphat A; 1.
DR PROSITE; PS00616; HIS ACID PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS ACID PHOSPHAT_2; 1.
KW Glycoprotein; Hydrolase; Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 467 3-Phytase A.
FT ACT_SITE 82 82 Nucleophile (By similarity).
FT ACT_SITE 362 362 Proton donor (By similarity).
FT DISULFID 31 40 By similarity.
FT DISULFID 71 414 By similarity.
FT DISULFID 215 465 By similarity.
FT DISULFID 264 282 By similarity.
FT DISULFID 436 444 By similarity.
FT CARBOHYD 27 27 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 59 59 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 105 105 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 120 120 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 207 207 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 230 230 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 339 339 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 352 352 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 376 376 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 388 388 N-linked (GLCNAC. .) (Potential).
SQ SEQUENCE 467 AA; 51074 MW; 1188828A5D7EC661 CRC64;

Query Match 97.9%; Score 2309; DB 1; Length 467;
Best Local Similarity 97.3%; Pred. No. 8.2e-164;
Matches 436; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 2 LAVPASRNSQSCDTVDQGYQCFSTSLWGQYAPFFSLANESVISPVPAGCRVTFQAQVL 61
DB 20 LAVPASRNSQSCDTVDQGYQCFSTSLWGQYAPFFSLANESVISPVPAGCRVTFQAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEEIQONATTPDGKVAFLKTYNSLGADDLTPFGQELVNS 121
DB 80 SRHGARYPTDSKGGKYSALIEEIQONATTPDGKVAFLKTYNSLGADDLTPFGQELVNS 139
QY 122 GIKFYQRYESLTRNIPFIRSSGSSRVASGKFIQGFQSTKLDPRAQCGQSSPKIDVV 181
DB 140 GIKFYQRYESLTRNIPFIRSSGSSRVASGKFIQGFQSTKLDPRAQCGQSSPKIDVV 199
QY 182 ISEASSNNLTDPGTCVFEDSELADTVEANFTATFVPSIRQRLNDSGLVTLTDTVTY 241
DB 200 ISEASSNNLTDPGTCVFEDSELADTVEANFTATFVPSIRQRLNDSGLVTLTDTVTY 259

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QY	242	LMDMCSFDTTSTSTVDTKLSFCDLFTHDEWINVDYLOSLLKKYYGHGAGNPLGPTQG	VGY	301
Db	260	LMDMCSFDTTSTSTVDTKLSFCDLFTHDEWINVDYLOSLLKKYYGHGAGNPLGPTQG	VGY	319
QY	302	ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSDHNGIIISILFALG	LYNGTK	361
Db	320	ANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSDHNGIIISILFALG	LYNGTK	379
QY	362	PLSTTTTVENTITQDGFSSAWTVPFASRLYVEMMQCAQEPLVRVLVNDRVVPLHGC	PCPD	421
Db	380	PLSTTTTVENTITQDGFSSAWTVPFASRLYVEMMQCAQEPLVRVLVNDRVVPLHGC	PCPD	439
QY	422	ALGRCRTDSFVRGLSFARSGGDWAECPA	449	
Db	440	ALGRCRTDSFVRGLSFARSGGDWAECSA	467	
RESULT 6				
Q8JZ55				
ID	Q8JZ55	PRELIMINARY;	PRT;	448 AA.
AC	Q8JZ55;			
DT	01-MAR-2003 (TRENBLrel. 23, Created)			
DT	01-MAR-2003 (TRENBLrel. 23, Last sequence update)			
DT	01-MAR-2004 (TRENBLrel. 26, Last annotation update)			
DE	Phytase (Fragment).			
GN	Name=phyA;			
OS	Aspergillus fumigum.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;			
OC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.			
OX	NCBI_TaxID=5058;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Li G., Zhu J., Sun J., Wu Z., Wang L., Chen G., Jiang H., Li M.;			
RL	Submitted (AUG-2002) to the EMBL/GenBank/DDJF databases.			
DR	EMBL; AF537344; AANI0115.1; -.			
DR	GO; GO:0003993; F:acid phosphatase activity; IEA.			
DR	InterPro: IPR000560; HisAc phosphase.			
DR	Pfam; PF00328; Acid_phosphat_A; 1.			
DR	PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.			
DR	PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.			
FT	NON TER			
SO	SEQUENCE	448 AA;	49260 MW;	0554FF9712FF7BAA CRC64;

Query Match	96.6%;	Score 2279;	DB 2;	Length 448;
Best Local Similarity	95.5%;	Pred. No. 1.3e-161;		
Matches 428;	Conservative 14;	Mismatches 6;	Indels 0;	Gaps 0;

Qy	2	LAVPASRNQSCDVTDGYQCFSTSHLWGQYAPFSLANESVTSPEVPACGRVTEAQLV	61
Db	1	LAVPASRNQSCDVTDGYQCFSTSHLWGQYAPFSLANKSAISPDVPACQVTFEQLV	60
Qy	62	SRHGARYPTDSKGKYGALIEEIQONATTPOCKYAFLLKTYNSLGADDLTPFGQEVLNS	121
Db	61	SRHGARYPTDSKGKYGALIEEIQONATTFEKKYAFLLKTYNSLGADDLTPFGQEVLNS	120
Qy	122	GIKFYQRYESLTRNIVFPIRSSGSSRVIASGKKTIEGFQSTKLDPRAQPCQSSPKIDW	181
Db	121	GVKFYQRYESLTRNIVFPIRSSGSSRVIASGKKTIEGFQSTKLDPRAQPCQSSPKIDW	180
Qy	182	ISEASSGNNTLDPGTCVTFEDELADVTEANFTATFVPSIQRLNDLSGVTLTDEVTY	241
Db	181	ISEASTGNNTLDPGTCVTFEDELADIEANFTATFVPSIQRLNDLSGVTLTDEVTY	240
Qy	242	LMDWCSEDTISTSTVDTKLSPFCDLFTHDEWINVDYQLSLKKYXGHGAGNLPGBTQGVY	301
Db	241	LMDWCSEDTISTSTVDTKLSPFCDLFTHDEWINVDYQLSLKNKYXGHGAGNLPGBTQGVY	300
Qy	302	ANELLIALRTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTK	361
Db	301	ANELLIALRTHSPVHDDTSSNHTLDSPATFPLNSTLYADFSDHNGIISILFALGLYNGTK	360
Qy	362	PLSTTTTVENITQTDFSSAWTVPFASRLYVEMWQCAEQEPLFRLVINDRVVPLHGCVD	421

Db	361	PLSSTTAENITQDGFSSAWTVPPASRMYVENMQQSEQEPFLVRVLVNDRVVPLHGCPVD	42
Qy	422	ALGRCRTRDSFVRGLSFARSGGDWAECEFA	449
Db	421	ALGRCRTRDSFVRGLSFARSGGDWAECEFA	448
RESULT 7			
Q6J336	Q6J336	PRELIMINARY; PRT; 448 AA.	
ID	Q6J336;		
AC	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Phytase (Fragment).		
DE	Aspergillus oryzae.		
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;		
OC	Euriales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.		
CX	NCBI_TaxID=5062;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Nong Y., He Y., Rachid L., Wu Z., Qing Y.;		
RL	Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY603416; AAT12504.1; -.		
DR	InterPro; IPR000560; HisAc_phsphtse.		
DR	Pfam; PF00328; Acid_phosphat_A; 1.		
DR	PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.		
DR	PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.		
FT	NON_TER		
SQ	SEQUENCE 448 AA; 49169 MW; FRABFCD20140514 CRC64;		
Query Match 96.6%; Score 2278; DB 2; Length 448;			
Best Local Similarity 95.3%; Pred. No. 1.6e-161;			
Matches 427; Conservative 14; Mismatches 7; Indels 0; Gaps 0;			
Qy	2	LAVPASRNOSSCDTVDQGYQCFSETSHLWGOYADPFSLANESVTSRVPAGCVRTPAQVL	61
Db	1	LAVPASRNOSSCDTVDQGYQCFSETSHLWGOYADPFSLANESVTSRVPAGCVRTPAQVL	60
Qy	62	SRHGARYPTDSKGKYSALIEIQONATTPGKYAFLKTYNSLGADLLTPGEQELVNS	121
Db	61	SRHGARYPTDSKGKYSALIEIQONATTPGKYAFLKTYNSLGADLLTPGEQELVNS	120
Qy	122	GIKFYQRYESLNRNTPVPIRSGSSSRVIASGKKTFIEGFQSTKLDPRAQPGQSSPKIDVV	181
Db	121	GKFKYQRYESLNRNTPVPIRSGSSSRVIASGKKTFIEGFQSTKLDPRAQPGQSSPKIDVV	180
Qy	182	ISEASSNNITLDPGCTVPEFSEADTVANFTATFVPSIRORLENDLSGVTITDTEVTY	241
Db	181	ISEASTNNITLDPGCTVPEFSEADTVANFTATFVPSIRORLENDLSGVTITDTEVTY	240
Qy	242	LMDMCSFDITSTSTVDTKLSFCOLFTHDEWINDYLSLKKYKHGAGNPLGPTQGVY	301
Db	241	LMDMCSFDITSTSTVDTKLSFCOLFTHDEWINDYLSLKKYKHGAGNPLGPTQGVY	300
Qy	302	ANELIARLTHSPVHDDTSSNHTLDSGPATFPINSLTVADFSHDNGIISILFALGLYNGTK	361
Db	301	ANELIARLTHSPVHDDTSSNHTLDSNPATFPINSLTVADFSHDNGIISILFALGLYNGTK	360
Qy	362	PLSTTTVENITQDGFSSAWTVPPASRMYVENMQQSEQEPFLVRVLVNDRVVPLHGCPVD	421
Db	361	PLSSTTAENITQDGFSSAWTVPPASRMYVENMQQSEQEPFLVRVLVNDRVVPLHGCPVD	420
Qy	422	ALGRCRTRDSFVRGLSFARSGGDWAECEFA	449
Db	421	ALGRCRTRDSFVRGLSFARSGGDWAECEFA	448

RESULT 8		
AAT12504		
ID	AAT12504	PRELIMINARY; PRT; 448 AA.
AC	AAT12504;	
DT	20-MAY-2004	(TREMELrel. 27, Created)

DT 20-MAY-2004 (TrEMBLrel. 27, Last sequence update)
 DE Phytase (Fragment).
 OS Aspergillus oryzae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Aspergillus.
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5062;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nong Y., He Y., Rachid L., Wu Z., Qing Y.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 FT EMBL; AY603416; AAT12504.1; -
 FT NON TER 1
 SQ SEQUENCE 448 AA; 49169 MW; FBABFCDE20140514 CRC64;

 Query Match 96.6%; Score 2278; DB 2; Length 448;
 Best Local Similarity 95.3%; Pred. No. 1.6e-161;
 Matches 427; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

 Qy 2 LAVPASRNQSSCDTVDQGYQCFSTSHLWQYAPFFSLANESVTSPEVPAGCRVTFPAQVL 61
 Db 1 LAVPASRNQSSCDTVDQGYQCFSTSHLWQYAPFFSLANESVTSPEVPAGCHVTFPAQVL 60

 Qy 62 SRHGARYPTDSKGGKYSALIBEIQQNATTFPGKYAFKTKYNSLGADDLTPFGQELVNS 121
 Db 61 SRHGARYPTDSKGGKYSALIBEIQQNATTFPGKYAFKTKYNSLGADDLTPFGQELVNS 120

 Qy 122 GIKFYQRYESLTRNIVPFIRSSGSRVIAAGKFFIEGFQSTKLDPRAPQSSPKIDVV 181
 Db 121 GIKFYQRYESLTRNIVPFIRSSGSRVIAAGKFFIEGFQSTKLDPRAPQSSPKIDVV 180

 Qy 182 ISRASSNNILDPGCTCVFEDSELADTVEANFTATFVPSIRQRLNDLSGVLTDTEVY 241
 Db 181 ISRASSNNILDPGCTCVFEDSELADTVEANFTATFVPSIRQRLNDLSGVLTDTEVY 240

 Qy 242 LMDMCSFDTTSTVDTKLSPFCDFLTHDEWINVDYLSLKKYKGAGNPLGPTQGVY 301
 Db 241 LMDMCSFDTTSTVDTKLSPFCDFLTHDEWINVDYLSLKKYKGAGNPLGPTQGVY 300

 Qy 302 ANELIARLTHSPVHDDTSSNHTLDSPPATPLNSTLYADFSDHNGIISILFALGLYNGTK 361
 Db 301 ANELIARLTHSPVHDDTSSNHTLDSPPATPLNSTLYADFSDHNGIISILFALGLYNGTK 360

 Qy 362 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRLVNDRVVPLHGCPVD 421
 Db 361 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRLVNDRVVPLHGCPVD 420

 Qy 422 ALGRCRDSFVRGLSFARSGDWAECFA 449
 Db 421 ALGRCRDSFVRGLSFARSGDWAECFA 448

 RESULT 9
 O93838 PRELIMINARY; PRT; 467 AA.
 ID O93838
 AC O93838
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DE 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Phytase.
 GN Name=PhyA;
 OS Aspergillus niger.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Aspergillus.
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5061;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nagashima T., Kondo H., Anazawa H., Terasaki Y.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 FT EMBL; AB022700; BAA74433.1; -
 DR HSP; P34752; 1IHP.
 DR GO; GO:0003993; F:acid phosphatase activity; IEA.

DR InterPro; IPR000560; HisAc phsptse.
 DR Pfam; PF00328; Acid phosphat A; 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 SQ SEQUENCE 467 AA; 51028 MW; 7A38AD543EDC265C CRC64;

 Query Match 96.6%; Score 2278; DB 2; Length 467;
 Best Local Similarity 95.3%; Pred. No. 1.7e-161;
 Matches 427; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

 Qy 2 LAVPASRNQSSCDTVDQGYQCFSTSHLWQYAPFFSLANESVTSPEVPAGCRVTFPAQVL 61
 Db 20 LAVPASRNQSSCDTVDQGYQCFSTSHLWQYAPFFSLANESVTSPEVPAGCHVTFPAQVL 79

 Qy 62 SRHGARYPTDSKGGKYSALIBEIQQNATTFPGKYAFKTKYNSLGADDLTPFGQELVNS 121
 Db 80 SRHGARYPTDSKGGKYSALIBEIQQNATTFPGKYAFKTKYNSLGADDLTPFGQELVNS 139

 Qy 122 GIKFYQRYESLTRNIVPFIRSSGSRVIAAGKFFIEGFQSTKLDPRAPQSSPKIDVV 181
 Db 140 GIKFYQRYESLTRNIVPFIRSSGSRVIAAGKFFIEGFQSTKLDPRAPQSSPKIDVV 199

 Qy 182 ISRASSNNILDPGCTCVFEDSELADTVEANFTATFVPSIRQRLNDLSGVLTDTEVY 241
 Db 200 ISRASSNNILDPGCTCVFEDSELADTVEANFTATFVPSIRQRLNDLSGVLTDTEVY 259

 Qy 242 LMDMCSFDTTSTVDTKLSPFCDFLTHDEWINVDYLSLKKYKGAGNPLGPTQGVY 301
 Db 260 LMDMCSFDTTSTVDTKLSPFCDFLTHDEWINVDYLSLKKYKGAGNPLGPTQGVY 319

 Qy 302 ANELIARLTHSPVHDDTSSNHTLDSPPATPLNSTLYADFSDHNGIISILFALGLYNGTK 361
 Db 320 ANELIARLTHSPVHDDTSSNHTLDSPPATPLNSTLYADFSDHNGIISILFALGLYNGTK 379

 Qy 362 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRLVNDRVVPLHGCPVD 421
 Db 380 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRLVNDRVVPLHGCPVD 439

 Qy 422 ALGRCRDSFVRGLSFARSGDWAECFA 449
 Db 440 ALGRCRDSFVRGLSFARSGDWAECFA 467

 RESULT 10
 O6GYA8 PRELIMINARY; PRT; 448 AA.
 ID O6GYA8
 AC O6GYA8
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Phytase (EC 3.1.3.8) (Fragment).
 GN Name=phyh;
 OS Aspergillus niger.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Aspergillus.
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5061;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N-2;
 RA Wu J., Yan C.Y.;
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY615712; AAT51735.1; -
 DR InterPro; IPR000560; HisAc phsptse.
 DR Pfam; PF00328; Acid phosphat A; 1.
 DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
 DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
 KW Hydrolase.
 FT NON TER 1
 SQ SEQUENCE 448 AA; 49170 MW; C319E1F3CEB4EF18 CRC64;

 Query Match 96.4%; Score 2273; DB 2; Length 448;
 Best Local Similarity 95.1%; Pred. No. 3.8e-161;
 Matches 426; Conservative 15; Mismatches 7; Indels 0; Gaps 0;

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QY 2 LAVPASRNOSSCDTVDQGYQCFSETSHLWGOYAPFFSLANESVISPVEPAGCRVTFAQVL 61
Db 1 LAVPASRNOSSCDTVDQGYQCFSETSHLWGOYAPFFSLANKSAISPDVPAGCHVTFAQVL 60
QY 62 SRHGARYPTDSKGGKYSALIEIQNATTFDGYAFLKTYNYSLGADDLTPFGEQELVNS 121
Db 61 SRHGARYPTDSKGGKYSALIEIQNATTFEGKYAFLKTYNYSLGADDLTPFGEQELVNS 120
QY 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGOSSPKIDVV 181
Db 121 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGOSSPKIDVV 180
QY 182 ISEASSNNLTDPGCTVFEDSELDATVEANFTATFVPSIRORLNDLSGVLTLTTEVTY 241
Db 181 ISEASTSNLTDPGCTVFEDSELDATVEANFTATFVPSIRORLNDLSGVLTLTTEVTY 240
QY 242 LMDMCSFDTISTSTVDTKLSPPCDLFTHEWINYDYLQSLKKYKYGAGNPLGPTQGVGY 301
Db 241 LMDMCSFDTISTSTVDTKLSPPCDLFTHEWINYDYLQSLKKYKYGAGNPLGPTQGVGY 300
QY 302 ANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 361
Db 301 ANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 360
QY 362 PLSTTTVENITQTDGFSSAWTVPPASRLYVENMQCAEQEPLRVVLVNDRVVPLHGCPVD 421
Db 361 PLSTTTAENITQTDGFSSAWTVPPASRLYVENMQCAEQEPLRVVLVNDRVVPLHGCPVD 420
QY 422 ALGRCRDSFVRGLSFARSGGDWAECEFA 449
Db 421 ALGRCRDSFVKGLSFARSGGDWAECEFA 448
QY 449 ALGRCRDSFVKGLSFARSGGDWAECEFA 448
Db 448 ALGRCRDSFVKGLSFARSGGDWAECEFA 448

RESULT 11
Q9HEQ0
ID Q9HEQ0 PRELIMINARY; PRT; 467 AA.
AC Q9HEQ0;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Phytase.
OS Aspergillus ficum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5038;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang L., An L., Wang Y., Yuan X.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY013315; AAG4085.1; -.
DR HSP; P34752; IHP.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc_phsphtse.
DR Pfam; PF00328; Acid_phosphat_A; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
SQ SEQUENCE 467 AA; 51012 MW; 3F69AD543C0B565B CRC64;

Query Match 96.2%; Score 2268; DB 2; Length 467;
Best Local Similarity 95.3%; Pred. No. 9.4e-161;
Matches 427; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 2 LAVPASRNOSSCDTVDQGYQCFSETSHLWGOYAPFFSLANESVISPVEPAGCRVTFAQVL 61
Db 20 LAVPASRNOSSCDTVDQGYQCFSETSHLWGOYAPFFSLANKSAISPDVPAGCHVTFAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEIQNATTFDGYAFLKTYNYSLGADDLTPFGEQELVNS 121
Db 80 SRHGARYPTDSKGGKYSALIEIQNATTFEGKYAFLKTYNYSLGADDLTPFGEQELVNS 139
QY 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGOSSPKIDVV 181
Db 121 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGOSSPKIDVV 180

Query Match 96.1%; Score 2265; DB 2; Length 467;
Best Local Similarity 95.1%; Pred. No. 1.6e-160;
Matches 426; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 2 LAVPASRNOSSCDTVDQGYQCFSETSHLWGOYAPFFSLANESVISPVEPAGCRVTFAQVL 61
Db 20 LAVPASRNOSSCDTVDQGYQCFSETSHLWGOYAPFFSLANKSAISPDVPAGCHVTFAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEIQNATTFDGYAFLKTYNYSLGADDLTPFGEQELVNS 121
Db 80 SRHGARYPTDSKGGKYSALIEIQNATTFEGKYAFLKTYNYSLGADDLTPFGEQELVNS 139
QY 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGOSSPKIDVV 181
Db 140 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGOSSPKIDVV 199
QY 182 ISEASSNNLTDPGCTVFEDSELDATVEANFTATFVPSIRORLNDLSGVLTLTTEVTY 241
Db 200 ISEASSNNLTDPGCTVFEDSELDATVEANFTATFVPSIRORLNDLSGVLTLTTEVTY 259
QY 242 LMDMCSFDTISTSTVDTKLSPPCDLFTHEWINYDYLQSLKKYKYGAGNPLGPTQGVGY 301
Db 260 LMDMCSFDTISTSTVDTKLSPPCDLFTHEWINYDYLQSLKKYKYGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 379

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Db 140 GVKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGOSSPKIDVV 199
QY 182 ISEASSNNLTDPGCTVFEDSELDATVEANFTATFVPSIRORLNDLSGVLTLTTEVTY 241
Db 200 ISEASTSNLTDPGCTVFEDSELDATVEANFTATFVPSIRORLNDLSGVLTLTTEVTY 259
QY 242 LMDMCSFDTISTSTVDTKLSPPCDLFTHEWINYDYLQSLKKYKYGAGNPLGPTQGVGY 301
Db 260 LMDMCSFDTISTSTVDTKLSPPCDLFTHEWINYDYLQSLKKYKYGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGFSSAWTVPPASRLYVENMQCAEQEPLRVVLVNDRVVPLHGCPVD 421
Db 380 PLSTTTAENITQTDGFSSAWTVPPASRLYVENMQCAEQEPLRVVLVNDRVVPLHGCPVD 439
QY 422 ALGRCRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGRCRDSFVKGLSFARSGGDWAECEFA 467

RESULT 12
Q6R519
ID Q6R519 PRELIMINARY; PRT; 467 AA.
AC Q6R519;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Phytase A.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Y., Wu Y., Che C.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY513749; AAS00648.1; -.
DR InterPro; IPR000560; HisAc_phsphtse.
DR Pfam; PF00328; Acid_phosphat_A; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
SQ SEQUENCE 467 AA; 51094 MW; 64AD085AB27AC099 CRC64;

Query Match 96.1%; Score 2265; DB 2; Length 467;
Best Local Similarity 95.1%; Pred. No. 1.6e-160;
Matches 426; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 2 LAVPASRNOSSCDTVDQGYQCFSETSHLWGOYAPFFSLANESVISPVEPAGCRVTFAQVL 61
Db 20 LAVPASRNOSSCDTVDQGYQCFSETSHLWGOYAPFFSLANKSAISPDVPAGCHVTFAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEIQNATTFDGYAFLKTYNYSLGADDLTPFGEQELVNS 121
Db 80 SRHGARYPTDSKGGKYSALIEIQNATTFEGKYAFLKTYNYSLGADDLTPFGEQELVNS 139
QY 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGOSSPKIDVV 181
Db 140 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGOSSPKIDVV 199
QY 182 ISEASSNNLTDPGCTVFEDSELDATVEANFTATFVPSIRORLNDLSGVLTLTTEVTY 241
Db 200 ISEASSNNLTDPGCTVFEDSELDATVEANFTATFVPSIRORLNDLSGVLTLTTEVTY 259
QY 242 LMDMCSFDTISTSTVDTKLSPPCDLFTHEWINYDYLQSLKKYKYGAGNPLGPTQGVGY 301
Db 260 LMDMCSFDTISTSTVDTKLSPPCDLFTHEWINYDYLQSLKKYKYGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 379

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QY 362 PLSTTTVENITQTDGSSAWTPVPASRLYYEMMQCAEQEFLVRLVNDVRVPLHGCPVD 421
 DB 380 PLSTTTAENITQTDGSSAWTPVPASRLYYEMMQCAEQEFLVRLVNDVRVPLHGCPAD 439

QY 422 ALGCTRDTSFVRLGSLFARSGGDWAECEFA 449

DB 440 ALGCTRDTSFVRLGSLFARSGGDWAECEFA 467

RESULT 13

AAS00648 PRELIMINARY; PRT; 467 AA.
 AC AAS00648;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DE Phytase A.
 GN PHYA.
 OS Aspergillus niger.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5061;
 RN [1]
 RP SEQUENCE FROM N.A.,
 RA Zhang Y., Wu Y., Che C.;
 RT "Aspergillus niger phytase."
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY513749; AAS00648.1;
 SQ SEQUENCE 467 AA; 51094 MW; 64AD06BAB27AC099 CRC64;

Query Match 96.1%; Score 2265; DB 2; Length 467;

Best Local Similarity 95.1%; Pred. No. 1.6e-160;

Matches 426; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 2 LAVPASNQSCDVTVDQGYQCFSETSLWQYAPFFSLANESVISPVPACRVTFAQVL 61
 DB 20 LAVPASNQSCDVTVDQGYQCFSETSLWQYAPFFSLANESVISPVPACRVTFAQVL 79

QY 62 SRHGARYPTDSKGKYSALIEEQONATTFDGKVAFLKTNYSGLGADLTPEGBOELVNS 121

DB 80 SRHGARYPTDSKGKYSALIEEQONATTFDGKVAFLKTNYSGLGADLTPEGBOELVNS 139

QY 122 GIKFYQYRESLTRNIPFIRSSGSSRRVIAAGKFFIEGFQSTKLKDPRAQCGQSPKIDVV 181

DB 140 GIKFYQYRESLTRNIPFIRSSGSSRRVIAAGKFFIEGFQSTKLKDPRAQCGQSPKIDVV 199

QY 182 ISEASSNNLTDPGTCVTFEDSELADTVANFTATVPSTRQRLNLSGVTLTDTETVY 241

DB 200 ISEASSNNLTDPGTCVTFEDSELADTVANFTATVPSTRQRLNLSGVTLTDTETVY 259

QY 242 LMDMCSFDTTISTVDPKLPFCDFLTHDEWINVDYLSLKKYGHGAGNPLGPTQGVY 301

DB 260 LMDMCSFDTTISTVDPKLPFCDFLTHDEWINVDYLSLKKYGHGAGNPLGPTQGVY 319

QY 302 ANELIARLTHSPVHDTSNHTLDSPPATPLNLTLYADFSDHNGIISILFALGLYNGTK 361

DB 320 ANELIARLTHSPVHDTSNHTLDSPPATPLNLTLYADFSDHNGIISILFALGLYNGTK 379

QY 362 PLSTTTVENITQTDGSSAWTPVPASRLYYEMMQCAEQEFLVRLVNDVRVPLHGCPVD 421

DB 380 PLSTTTAENITQTDGSSAWTPVPASRLYYEMMQCAEQEFLVRLVNDVRVPLHGCPAD 439

QY 422 ALGCTRDTSFVRLGSLFARSGGDWAECEFA 449

DB 440 ALGCTRDTSFVRLGSLFARSGGDWAECEFA 467

RESULT 14

PHYA ASPFU
 ID PHYA ASPFU
 AC O00092; PRT; 465 AA.

DT 29-MAR-2004 (Rel. 43, Created)

DT

29-MAR-2004 (Rel. 43, Last sequence update)

DT

05-JUL-2004 (Rel. 44, Last annotation update)

DE

3-phytase A precursor (EC 3.1.3.8) (Myo-inositol-hexakisphosphate 3-phosphohydrolase A) (3 phytase A) (Myo-inositol hexakisphosphate phosphohydrolase A).

DE

Name=PHYA;

OS

Aspergillus fumigatus (Sartorya fumigata).

OC

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

OX

NCBI_TaxID=5085;

RN

SEQUENCE FROM N.A., SEQUENCE OF 27-37, AND CHARACTERIZATION.

RP

STRAIN=ATCC 34625;

RC

MEDLINE=97288063; PubMed=9143104;

RA

Parasomontes L., Haiker M., Wyss M., Tessier M., van Loon A.P.G.M.;

RT

"Gene cloning, purification, and characterization of a heat-stable

RT

phytase from the fungus Aspergillus fumigatus."

RL

Appl. Environ. Microbiol. 63:1696-1700(1997).

CC

FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

CC

from phytate.

CC

FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

CC

from phytate.

CC

FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

CC

from phytate.

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FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

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from phytate.

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FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

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from phytate.

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FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

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from phytate.

CC

FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

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from phytate.

CC

FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

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CC

FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

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from phytate.

CC

FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

CC

from phytate.

CC

FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

CC

from phytate.

CC

FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

CC

from phytate.

CC

FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

CC

from phytate.

CC

FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

CC

from phytate.

CC

FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

CC

from phytate.

CC

FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

CC

from phytate.

CC

FUNCTION: Catalyzes the hydrolysis of inorganic orthophosphate

Db 80 RHGARYPTSSKSKYKLVTAIQANATDFKGFAPLTKYNTYTLGADLLTPFGEOQLVNSG 139
QY 123 IKFYORYESLRNIVPFIIRSSGSSRVIASGKFFIEGFQSTKLKDPRAQPGQSSPKIDVVI 182
Db 140 IKFYQRYKALARSVVVPIIRASGSDRVIASGKFFIEGFQOAKIADPGA-TNRAAPAI SVII 198
QY 183 SEASSNNLTDPGTCVTFEDSELDATVEANFTATVPISIRQLENDLSGVTLTDEVTYL 242
Db 199 PESEFTFNLTGHVCTKFEASQLGDEVAANFTALPAPDIRABAEXHLPGVTLTDEDVVSL 258
QY 243 MDMCSFDITSTVDTKLSPPFCDLFTHDEWINYDLSKLYKHGAGNPLGPTQGVYANELI 306
Db 259 MDMCSFDIVARTSDASQLSPFCALFTQBEWAQYDYLQSVSKYGYGGNPLGPAQOIGFANELI 323
QY 303 NELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADPFSHONGIISILFALGLYNGTKP 362
Db 319 NELIARLTHSPVQDHTSNHTLDSSPATFPLNSTLYADPFSHONGIISILFALGLYNGTEP 378
QY 363 LSTTVENITQTDGFSSAWTVPFASRLYVEMMQCAEQBPVLRVLVNDRVVPLHGPCVDALGRC 426
Db 379 LSRTSVESAKELDGYASWVVPFGARAYFEITWQCKSEKEFLVRALINDRVVPLHGCVDK 438
QY 423 LGRCTRDSFVRGLSFARSGGDWAECEFA 449
Db 439 LGRCKLNDVFKGLSWARSGGNWGECEFS 465

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AC Q9C1T1; 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Phytase.
GN Name=phyA;
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RA Gomi K.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB042805; BAB40715.1; -
DR HSP; P34752; 11HP.
DR GO; GO:0003993; P:acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc.phsptase.
DR Pfam; PF00328; Acid_phosphat_A; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN 1.
SQ SEQUENCE 466 AA, 51257 MW, 8033BED57FBA2791 CRC64;

Query Match 68.3%; Score 1610; DB 2; Length 466;
Best Local Similarity 67.0%; Pred. No. 1.3e-111;
Matches 297; Conservative 57; Mismatches 89; Indels 0; Gaps 0;
QY 7 SRNQSCTVDQGYQCFSTSLWGQYAPFFSLANESVISPVPAGCRVTFPAQVLSRHGA 66
Db 24 SPQQSCNTVDQGYQCFSGVSLWGQYSPYFSDDESSLSDVDPDHCQVTFPAQVLSRHGA 83
QY 67 RYPTDSKGYKYSALIEICQNAFTDGVKVAFLKTYNSLGADLLTPFGEOQLVNSGIKFY 126
Db 84 RYPTKSKSEYAKLKVQHNATFSQKVAFLKSYNSLGADLLTPFGENQLVDSGIKFY 143
QY 127 QRYESITRNIVPFIIRSSGSSRVIASGKFFIEGFQSTKLKDPRAQPGQSSPKIDVWISAS 186
Db 144 QRYEELAKNVVPIIRASGSDRVIASGKFFIEGFQKAKLGDSKSKRGQAPIVNVVITETE 203
QY 187 SSNTLDPGTCVTFEDELADTVEANFTATVPISIRQLENDLSGVTLTDEVTYLMDMC 246
Db 204 GFNNTLHSLCTAFENSTTGDAEDKFTAVFTVPSIVERLEKDLPGTTLSSKEVVYLMDC 263

QY 247 SFDITSTVDTKLSPPFCDLFTHDEWINYDLSKLYKHGAGNPLGPTQGVYANELI 306
Db 264 SFDITLALTRDGSRLSPFCALFTQBEWAQYDYLQSVSKYGYGGNPLGPAQOIGFANELI 323
QY 307 ARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADPFSHONGIISILFALGLYNGTKP 366
Db 324 ARLTKSPVKDHTTNTTLDSPNATFPLNATLYADPFSHONTMTSVFALGLYNTTTFELSQ 383
QY 367 TVENITQTDGFSSAWTVPFASRLYVEMMQCAEQBPVLRVLVNDRVVPLHGPCVDALGRC 426
Db 384 SVQSTEETNGYSSARTVFPGARAYVEMMQCTDEKEPLVRVLVNDRVIFLQGCCDADEYGR 443
QY 427 TRDSFVRGLSFARSGGDWAECEFA 449
Db 444 KRDDFVEGLSFVTSGGNWGECEFA 466

Search completed: October 24, 2004, 12:58:05
Job time : 139 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 24, 2004, 11:28:49 ; Search time 54 Seconds
(without alignments)
551.422 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

Sequence: 1 MLAVASRNQSSCDTVDQY.....SFVRGLSPARSGDWAECFA 449

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/protdata/1/1aa/5B_COMB.pep:**

3: /cgn2_6/protdata/1/1aa/6A_COMB.pep:**

4: /cgn2_6/protdata/1/1aa/6B_COMB.pep:**

5: /cgn2_6/protdata/1/1aa/PCTUS_COMB.pep:**

6: /cgn2_6/protdata/1/1aa/backfiles1.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2353	99.8	467	1 US-08-151-574-32	Sequence 32, Appl
2	2353	99.8	467	1 US-08-146-424-20	Sequence 20, Appl
3	2353	99.8	467	1 US-08-693-709-2	Sequence 2, Appl
4	2353	99.8	467	2 US-08-419-448-32	Sequence 32, Appl
5	2353	99.8	467	2 US-08-819-825-3	Sequence 3, Appl
6	2353	99.8	467	3 US-09-163-642-3	Sequence 3, Appl
7	2353	99.8	467	3 US-09-233-510-32	Sequence 32, Appl
8	2353	99.8	467	4 US-09-636-499-5	Sequence 5, Appl
9	2341	99.3	467	4 US-09-273-871A-11	Sequence 11, Appl
10	2341	99.3	467	4 US-10-083-452-11	Sequence 11, Appl
11	2334	99.0	444	3 US-09-044-718-1	Sequence 1, Appl
12	2334	99.0	444	4 US-10-062-848-1	Sequence 1, Appl
13	2321	98.4	441	4 US-09-684-855-105	Sequence 105, Appl
14	2321	98.4	441	4 US-09-684-855-127	Sequence 127, Appl
15	2321	98.4	441	4 US-09-684-855-150	Sequence 150, Appl
16	2321	98.4	441	4 US-09-684-855-150	Sequence 150, Appl
17	2321	98.4	441	4 US-09-488-265B-5	Sequence 5, Appl
18	2309	97.9	467	1 US-07-923-724-8	Sequence 8, Appl
19	2309	97.9	467	2 US-08-609-426A-8	Sequence 8, Appl
20	2309	97.9	467	2 US-08-374-652C-2	Sequence 2, Appl
21	2288	97.0	441	4 US-09-684-855-104	Sequence 104, Appl
22	2288	97.0	441	4 US-09-684-855-149	Sequence 149, Appl
23	2288	97.0	441	4 US-09-488-265B-4	Sequence 4, Appl
24	2278	96.6	467	3 US-09-155-855-3	Sequence 3, Appl
25	2278	96.6	467	3 US-09-543-744-3	Sequence 3, Appl
26	2278	96.6	467	4 US-09-929-060-3	Sequence 3, Appl
27	2277	96.6	441	4 US-09-684-855-103	Sequence 103, Appl

28	2277	96.6	441	4 US-09-684-855-126	Sequence 126, Appl
29	2277	96.6	441	4 US-09-684-855-148	Sequence 148, Appl
30	2277	96.6	441	4 US-09-488-265B-3	Sequence 3, Appl
31	2255	95.6	443	3 US-09-155-855-1	Sequence 1, Appl
32	2255	95.6	443	3 US-09-543-744-1	Sequence 1, Appl
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37	1990	84.4	410	4 US-09-636-499-11	Sequence 11, Appl
38	1932	81.9	467	4 US-09-684-855-167	Sequence 167, Appl
39	1929	81.8	467	4 US-09-488-265B-35	Sequence 35, Appl
40	1833	77.7	467	4 US-09-684-855-161	Sequence 161, Appl
41	1833	77.7	467	4 US-09-488-265B-29	Sequence 29, Appl
42	1828	77.5	467	4 US-09-488-265B-91	Sequence 91, Appl
43	1822	77.3	467	4 US-09-488-265B-93	Sequence 93, Appl
44	1820	77.2	441	4 US-09-488-265B-24	Sequence 24, Appl
45	1820	77.2	467	4 US-09-684-855-139	Sequence 139, Appl

ALIGNMENTS

RESULT 1
US-08-151-574-32
; Sequence 32, Application US/08151574
; Patent No. 5436156
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Seltin
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-151-574-32
Query Match 99.8%; Score 2353; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 9e-235;

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QY	2	LAVPASRNQSSCCTVDQGYQCFSETSHLWGQYAPFFSLANESVISPVPAGRCVTFQAQVL	61		
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QY	62	SRHGARYPTDSKGKKYSALIEEIQONATTFPGKYAFILKTNYSLGADLTFPGQELVNS	121		
Db	80	SRHGARYPTDSKGKKYSALIEEIQONATTFPGKYAFILKTNYSLGADLTFPGQELVNS	139		
QY	122	GKIFYQRYESLTRNIVFFIRSSGSSRVIASGKKEIEGFQSTKLDPRAQPCQSSPKIDW	181		
Db	140	GKIFYQRYESLTRNIVFFIRSSGSSRVIASGKKEIEGFQSTKLDPRAQPCQSSPKIDW	199		
QY	182	ISEASSNNLTDPGCTCFVFDSELDATVEANFTATFVPSIRQRLENDLSGVTLTDTTEVY	241		
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Db	260	LMDCMSPDITISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYCHGAGNELPGTQGVGY	319		
QY	302	ANELIARLTHSPVHDDTSSNHTLDSSPATPPLNSTLYADFSHDNGIITISILFALGIYNGTK	361		
Db	320	ANELIARLTHSPVHDDTSSNHTLDSSPATPPLNSTLYADFSHDNGIITISILFALGIYNGTK	379		
QY	362	PLSTTTIVENTTQTDGFSASMTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD	421		
Db	380	PLSTTTIVENTTQTDGFSASMTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD	439		
QY	422	ALGRCTSDSFVRGLSFARSGGDWAECA	449		
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RESULT 2

US-08-146-424-20
Sequence 20, Application US/08146424
Patent No. 5593963
GENERAL INFORMATION:
APPLICANT: VAN OOLJEN, ALBERT J. J.
APPLICANT: RIETVELD, KRIJN
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: PEN, JAN
APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWOERD, TEUNIS C.
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,424
FILING DATE: 02-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KENNEDY, BILL
REGISTRATION NUMBER: 33,407
REFERENCE/DOCKET NUMBER: 44615-20011.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEO ID NO: 20:


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; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146,424
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20011.10
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Signal Sequence
; LOCATION: 1...23
; OTHER INFORMATION:
US-08-693-709-2

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Best Local Similarity 100.0%; Pred. No. 9e-235;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 80 SRHGARYPTDSKGYKSALIEIQONATTFDQKYAFKTYNYSGLGADDLTPFGEQELVNS 139

QY 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDKPRAQPGOSSPKIDVV 181
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DB 200 ISEASSNNLTDPGCTCTVFEDSELADTVFVPSIRQRLNDLSGVTLTDEVTY 259

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QY 362 PLSTTTVENITQDGFSSAWTVPFASRLYVENMQCAEQEPLRVLRVLRVLRVLRVLRVLRVLRV 421
DB 380 PLSTTTVENITQDGFSSAWTVPFASRLYVENMQCAEQEPLRVLRVLRVLRVLRVLRVLRVLRV 439

QY 422 ALGRCTRDSFVRGLSFARSGGDWAECA 449
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RESULT 4

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US-08-419-448-32
; Sequence 32, Application US/08419448
; Patent No. 5863533
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gortcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin

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; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,448
; FILING DATE: 10-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-419-448-32

Query Match 99.8%; Score 2353; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 9e-235;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTDVQGYQCFSESHLWQYAPFFSLANESVISPEVPAGCRVTFAQVL 61
DB 20 LAVPASRNQSSCDTDVQGYQCFSESHLWQYAPFFSLANESVISPEVPAGCRVTFAQVL 79

QY 62 SRHGARYPTDSKGYKSALIEIQONATTFDQKYAFKTYNYSGLGADDLTPFGEQELVNS 121
DB 80 SRHGARYPTDSKGYKSALIEIQONATTFDQKYAFKTYNYSGLGADDLTPFGEQELVNS 139

QY 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDKPRAQPGOSSPKIDVV 181
DB 140 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLDKPRAQPGOSSPKIDVV 199

QY 182 ISEASSNNLTDPGCTCTVFEDSELADTVFVPSIRQRLNDLSGVTLTDEVTY 241
DB 200 ISEASSNNLTDPGCTCTVFEDSELADTVFVPSIRQRLNDLSGVTLTDEVTY 259

QY 242 LMDMCSFDTISTSTVDTKLSPPCDLFTHDEWINYDYLQSLKYYGHGAGNPLGPTQGVGY 301
DB 260 LMDMCSFDTISTSTVDTKLSPPCDLFTHDEWINYDYLQSLKYYGHGAGNPLGPTQGVGY 319

QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATFPPLNSTLYADFSDHNGIISILFALGLYNGTK 361
DB 320 ANELIARLTHSPVHDDTSSNHTLDSPPATFPPLNSTLYADFSDHNGIISILFALGLYNGTK 379

QY 362 PLSTTTVENITQDGFSSAWTVPFASRLYVENMQCAEQEPLRVLRVLRVLRVLRVLRVLRVLRV 421
DB 380 PLSTTTVENITQDGFSSAWTVPFASRLYVENMQCAEQEPLRVLRVLRVLRVLRVLRVLRVLRV 439

QY 422 ALGRCTRDSFVRGLSFARSGGDWAECA 449
DB 440 ALGRCTRDSFVRGLSFARSGGDWAECA 467

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RESULT 5

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US-08-819-825-3
; Sequence 3, Application US/08819825
; Patent No. 5866118
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Ray, Michael W.
; APPLICANT: Klotz, Alan V.
; TITLE OF INVENTION: Polypeptides Having Phytase Activity
; TITLE OF INVENTION: And Nucleic Acids Encoding Same
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5866118o No. 5866118disk of No. 5866118th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,825
; FILING DATE: 18-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Labiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4758.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-819-825-3

Query Match          99.8%; Score 2353; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 9e-235;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LAVPASRNSQSCDVTQGYQCFSETSHLWQYAPFFPSLANESVISPEVPAGCRVTFQAVL 61
DB      20 LAVPASRNSQSCDVTQGYQCFSETSHLWQYAPFFPSLANESVISPEVPAGCRVTFQAVL 79

QY      62 SRGARYPTDSKGKYSALIEEQONATTFDGKYAFKTYNSLGLADDLTPFGEQELVNS 121
DB      80 SRGARYPTDSKGKYSALIEEQONATTFDGKYAFKTYNSLGLADDLTPFGEQELVNS 139

QY      122 GIKFYQRYESLNRNIVPFRSSGSSRVIASGKKPIEGFQSTKLKDPRAQPGQSSPKIDVV 181
DB      140 GIKFYQRYESLNRNIVPFRSSGSSRVIASGKKPIEGFQSTKLKDPRAQPGQSSPKIDVV 199

QY      182 ISSEASSNNLDPGTCVTFEDSELADTVANFTATFVPSIRQRLNDSGLVTLTDTEVTY 241
DB      200 ISSEASSNNLDPGTCVTFEDSELADTVANFTATFVPSIRQRLNDSGLVTLTDTEVTY 259

QY      242 LMDMCSFDTTISTVDTKLSPPFCDLFTHDEWINYDIQSLKKYKGAGNPLGPTQGVG 301
DB      260 LMDMCSFDTTISTVDTKLSPPFCDLFTHDEWINYDIQSLKKYKGAGNPLGPTQGVG 319

US-09-163-642-3
; Sequence 3, Application US/09163642
; Patent No. 6221644
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Ray, Michael W.
; APPLICANT: Klotz, Alan V.
; TITLE OF INVENTION: Polypeptides Having Phytase Activity
; TITLE OF INVENTION: And Nucleic Acids Encoding Same
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6221644o No. 6221644disk of No. 6221644th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/163,642
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,825
; FILING DATE: 18-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Labiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4758.200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-163-642-3

Query Match          99.8%; Score 2353; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 9e-235;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 LAVPASRNSQSCDVTQGYQCFSETSHLWQYAPFFPSLANESVISPEVPAGCRVTFQAVL 61
DB      20 LAVPASRNSQSCDVTQGYQCFSETSHLWQYAPFFPSLANESVISPEVPAGCRVTFQAVL 79

QY      62 SRGARYPTDSKGKYSALIEEQONATTFDGKYAFKTYNSLGLADDLTPFGEQELVNS 121
DB      80 SRGARYPTDSKGKYSALIEEQONATTFDGKYAFKTYNSLGLADDLTPFGEQELVNS 139

QY      122 GIKFYQRYESLNRNIVPFRSSGSSRVIASGKKPIEGFQSTKLKDPRAQPGQSSPKIDVV 181
DB      140 GIKFYQRYESLNRNIVPFRSSGSSRVIASGKKPIEGFQSTKLKDPRAQPGQSSPKIDVV 199

QY      182 ISSEASSNNLDPGTCVTFEDSELADTVANFTATFVPSIRQRLNDSGLVTLTDTEVTY 241
DB      200 ISSEASSNNLDPGTCVTFEDSELADTVANFTATFVPSIRQRLNDSGLVTLTDTEVTY 259

QY      242 LMDMCSFDTTISTVDTKLSPPFCDLFTHDEWINYDIQSLKKYKGAGNPLGPTQGVG 301
DB      260 LMDMCSFDTTISTVDTKLSPPFCDLFTHDEWINYDIQSLKKYKGAGNPLGPTQGVG 319
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QY	302	ANELIAELTHSPVHDDTSSNHTLSSPATPPLNSTLYADFSDNGNGIIILFALGHYNGTK	361
Db	320	ANELIAELTHSPVHDDTSSNHTLSSPATPPLNSTLYADFSDNGNGIIILFALGHYNGTK	379
QY	362	PLSTTTVENTITQDGFSSAWTPFASRLYVEMMCOAQEQEPLRVLVNDRVVPLHGCPVD	421
Db	380	PLSTTTVENTITQDGFSSAWTPFASRLYVEMMCOAQEQEPLRVLVNDRVVPLHGCPVD	439
QY	422	ALGCRTRDSFVRGLSFARSGGDWAECEFA	449
Db	440	ALGCRTRDSFVRGLSFARSGGDWAECEFA	467

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RESULT 7
US-09-233-510-32
; Sequence 32, Application US/092333510
; Patent No. 6350602
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,510
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-233-510-32

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Db	80	SRHGARYPTDSGKKYSALIEBILQONATTFDGGYAFKTYNYSLGADDLTPFGEQELVNS	139	
Qy	122	GKIFYQRYESLTENIVPFFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAPQGSSPKIDVV	181	
Db	140	GKIFYQRYESLTENIVPFFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAPQGSSPKIDVV	199	
Qy	182	ISASSSNNLTDPGCTCTVEDSELADTVBANFATVPISIRQLENLDSGVLTDTEVTY	241	
Db	200	ISEASSSNNLTDPGCTCTVEDSELADTVBANFATVPISIRQLENLDSGVLTDTEVTY	259	
Qy	242	LMDMCSFDFIISTVDTKLSPFCDLTFHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVY	301	
Db	260	LMDMCSFDFIISTVDTKLSPFCDLTFHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVY	319	
Qy	302	ANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLIYADFSDHNGHISILFALGLYNGTK	361	
Db	320	ANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLIYADFSDHNGHISILFALGLYNGTK	379	
Qy	362	PLSTTTTVENITQDGFSSAWTVFFASRLYVEMMQCAQEPLVRVLVNDRVVPLHGPCVD	421	
Db	380	PLSTTTTVENITQDGFSSAWTVFFASRLYVEMMQCAQEPLVRVLVNDRVVPLHGPCVD	439	
Qy	422	ALGCRTRDSFVRGLSFARSGDWAECFA	449	
Db	440	ALGCRTRDSFVRGLSFARSGDWAECFA	467	
RESULT 8				
US-09-636-499-5				
; Sequence 5, Application US/09636499				
; Patent No. 6475762				
; GENERAL INFORMATION:				
; APPLICANT: Stafford, Christian F.				
; APPLICANT: Trinci, Anthony P.J.				
; APPLICANT: Brookman, Jayne L.				
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding			Incorporating Same	
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding				
; FILE REFERENCE: GC586-2				
; CURRENT APPLICATION NUMBER: US/09/636,499				
; CURRENT FILING DATE: 2000-08-11				
; PRIOR APPLICATION NUMBER: US 60/148,960				
; PRIOR FILING DATE: 1999-08-13				
; NUMBER OF SEQ ID NOS: 34				
; SOFTWARE: FastSeq for Windows Version 4.0				
; SEQ ID NO 5				
; LENGTH: 467				
; TYPE: PRT				
; ORGANISM: Aspergillus niger				
US-09-636-499-5				

Query Match	99.8%;	Score 2353;	DB 4;	Length 467;
Best Local Similarity	100.0%;	Pred. No. 9e-235;		
Matches 448;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	2	LAVPAGRNOSCDTVDQGYQCFSETHLMGQYAPFFSLANESVISPEVAGACRVTPAQVL	61	
Db	20	LAVPAGRNOSCDTVDQGYQCFSETHLMGQYAPFFSLANESVISPEVAGACRVTPAQVL	79	
Qy	62	SREGARYPTDSKGKYSALIEEQQNATTFDGKYAFKTVNYSLGADDTTPFGEQBLVNS	121	
Db	80	SREGARYPTDSKGKYSALIEEQQNATTFDGKYAFKTVNYSLGADDTTPFGEQBLVNS	139	
Qy	122	GIFYQRYESLTENIVPFISSGSSRVIASGKKFIEGFQSTKLDPRAPOGSSPKIDVW	181	
Db	140	GIFYQRYESLTENIVPFISSGSSRVIASGKKFIEGFQSTKLDPRAPOGSSPKIDVW	199	
Qy	182	ISEASSNNLTDPGCTCTVEDSELADTVEANFTATVPFSIRQLENDLSGVLTDTDEVY	241	
Db	200	ISEASSNNLTDPGCTCTVEDSELADTVEANFTATVPFSIRQLENDLSGVLTDTDEVY	259	
Qy	242	LMDMCSFDITSTSTVDTKLSPFCDLTFHDEWINDYLOSLKKYHYGHGAGNLPGTQGVY	301	
Db	260	LMDMCSFDITSTSTVDTKLSPFCDLTFHDEWINDYLOSLKKYHYGHGAGNLPGTQGVY	319	

QY 302 ANELIARLTHSPVHDDTSSNHTLDSSTPATPLNSTLYADFSHDNGIISILFALGLYNGTK 361
DB 320 ANELIARLTHSPVHDDTSSNHTLDSSTPATPLNSTLYADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGFSSAMTVPFASRLYVEMMQCAEQAPLVRVLVNDRVVPLHGCPVD 421
DB 380 PLSTTTVENITQTDGFSSAMTVPFASRLYVEMMQCAEQAPLVRVLVNDRVVPLHGCPVD 439
QY 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
DB 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 9
US-09-273-871A-11
; Sequence 11, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273.871A
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus ficum
US-09-273-871A-11

Query Match 99.3%; Score 2341; DB 4; Length 467;
Best Local Similarity 99.6%; Pred. No. 1.6e-233;
Matches 446; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 LAVPASRNQSSCDTVDQGYQCFSTSHLWQYAPFFPSLANESVISPEVPAGCRVTFPAQVL 61
DB 20 LAVPASRNQSSCDTVDQGYQCFSTSHLWQYAPFFPSLANESVISPEVPAGCRVTFPAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEEIQONATTDPGKYAFIKTYNYSLGADDLTPFGQEQLVNS 121
DB 80 SRHGARYPTDSKGGKYSALIEEIQONATTDPGKYAFIKTYNYSLGADDLTPFGQEQLVNS 139
QY 122 GIKFYQYESTRNIVPFIRSSGSSRVIASGKKEIEGFSQTKLDPRAQPGQSSPKIDVV 181
DB 140 GIKFYQYESTRNIVPFIRSSGSSRVIASGKKEIEGFSQTKLDPRAQPGQSSPKIDVV 199
QY 182 ISBASSNNLTDPGTCVTFEDSELADTVEANFTATFVPSIRQRLNDSGLVTLTDEVTY 241
DB 200 ISBASSNNLTDPGTCVTFEDSELADTVEANFTATFVPSIRQRLNDSGLVTLTDEVTY 259
QY 242 LMDWCSPTTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYKYGAGNPLGPTQGVY 301
DB 260 LMDWCSPTTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYKYGAGNPLGPTQGVY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSSTPATPLNSTLYADFSHDNGIISILFALGLYNGTK 361
DB 320 ANELIARLTHSPVHDDTSSNHTLDSSTPATPLNSTLYADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGFSSAMTVPFASRLYVEMMQCAEQAPLVRVLVNDRVVPLHGCPVD 421
DB 380 PLSTTTVENITQTDGFSSAMTVPFASRLYVEMMQCAEQAPLVRVLVNDRVVPLHGCPVD 439
QY 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449

DB 380 PLSTTTVENITQTDGFSSAMTVPFASRLYVEMMQCAEQAPLVRVLVNDRVVPLHGCPVD 439
QY 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
DB 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467
RESULT 10
US-10-083-452-11
; Sequence 11, Application US/10083452
; Patent No. 6689358
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083.452
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273.871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus ficum
US-10-083-452-11

Query Match 99.3%; Score 2341; DB 4; Length 467;
Best Local Similarity 99.6%; Pred. No. 1.6e-233;
Matches 446; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 LAVPASRNQSSCDTVDQGYQCFSTSHLWQYAPFFPSLANESVISPEVPAGCRVTFPAQVL 61
DB 20 LAVPASRNQSSCDTVDQGYQCFSTSHLWQYAPFFPSLANESVISPEVPAGCRVTFPAQVL 79
QY 62 SRHGARYPTDSKGGKYSALIEEIQONATTDPGKYAFIKTYNYSLGADDLTPFGQEQLVNS 121
DB 80 SRHGARYPTDSKGGKYSALIEEIQONATTDPGKYAFIKTYNYSLGADDLTPFGQEQLVNS 139
QY 122 GIKFYQYESTRNIVPFIRSSGSSRVIASGKKEIEGFSQTKLDPRAQPGQSSPKIDVV 181
DB 140 GIKFYQYESTRNIVPFIRSSGSSRVIASGKKEIEGFSQTKLDPRAQPGQSSPKIDVV 199
QY 182 ISBASSNNLTDPGTCVTFEDSELADTVEANFTATFVPSIRQRLNDSGLVTLTDEVTY 241
DB 200 ISBASSNNLTDPGTCVTFEDSELADTVEANFTATFVPSIRQRLNDSGLVTLTDEVTY 259
QY 242 LMDWCSPTTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYKYGAGNPLGPTQGVY 301
DB 260 LMDWCSPTTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYKYGAGNPLGPTQGVY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSSTPATPLNSTLYADFSHDNGIISILFALGLYNGTK 361
DB 320 ANELIARLTHSPVHDDTSSNHTLDSSTPATPLNSTLYADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGFSSAMTVPFASRLYVEMMQCAEQAPLVRVLVNDRVVPLHGCPVD 421
DB 380 PLSTTTVENITQTDGFSSAMTVPFASRLYVEMMQCAEQAPLVRVLVNDRVVPLHGCPVD 439
QY 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449

Db 440 ALGCRTRDSFVRGLSFARSGGDWAECA 467
|||||

RESULT 11

US-09-044-718-1
; Sequence 1, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-09-044-718-1

Query Match 99.0%; Score 2334; DB 3; Length 444;
Best Local Similarity 100.0%; Pred. No. 7.7e-233;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ASRNQSSCDTVDQGYQCFSETSHLWGOYAPFFSLANESVISPEVAGCRVTPAQVLSRHG 65
Db 1 ASRNQSSCDTVDQGYQCFSETSHLWGOYAPFFSLANESVISPEVAGCRVTPAQVLSRHG 60
QY 66 ARYPDTSKGKYSALIEIQONATTFDGKYAPLKTNYNSLGGADLTTPFGEQELVNSGKIF 125
Db 61 ARYPDTSKGKYSALIEIQONATTFDGKYAPLKTNYNSLGGADLTTPFGEQELVNSGKIF 120
QY 126 YQRYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLKPRAQPGQSSPKIDVWVISEA 185
Db 121 YQRYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLKPRAQPGQSSPKIDVWVISEA 180
QY 186 SSSNNTLDPGCTVPEDESADTVEANFTATVPFVPSIRQLENDLSGVTLTDTTEVTYLMDM 245
Db 181 SSSNNTLDPGCTVPEDESADTVEANFTATVPFVPSIRQLENDLSGVTLTDTTEVTYLMDM 240
QY 246 CSFDTISTSTVDTKLSPFCDLTFHDEWINYDLSLKKYKGAGNPLGPTQGVGYANEL 305
Db 241 CSFDTISTSTVDTKLSPFCDLTFHDEWINYDLSLKKYKGAGNPLGPTQGVGYANEL 300
QY 306 IARLTHSPVHDDTSNHTLSDSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 365
Db 301 IARLTHSPVHDDTSNHTLSDSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 360
QY 366 TTVENITQDGFSSAWTVPFASRLYVENMQCOAEQELVRLVNDRVVPLHGPCVDALGR 425
Db 361 TTVENITQDGFSSAWTVPFASRLYVENMQCOAEQELVRLVNDRVVPLHGPCVDALGR 420
QY 426 CTRDSFVRGLSFARSGGDWAECA 449
Db 421 CTRDSFVRGLSFARSGGDWAECA 444

RESULT 12

US-10-062-848-1
; Sequence 1, Application US/10062848
; Patent No. 6734004
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis

; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-062-848-1
Query Match 99.0%; Score 2334; DB 4; Length 444;
Best Local Similarity 100.0%; Pred. No. 7.7e-233;
Matches 444; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ASRNQSSCDTVDQGYQCFSETSHLWGOYAPFFSLANESVISPEVAGCRVTPAQVLSRHG 65
Db 1 ASRNQSSCDTVDQGYQCFSETSHLWGOYAPFFSLANESVISPEVAGCRVTPAQVLSRHG 60
QY 66 ARYPDTSKGKYSALIEIQONATTFDGKYAPLKTNYNSLGGADLTTPFGEQELVNSGKIF 125
Db 61 ARYPDTSKGKYSALIEIQONATTFDGKYAPLKTNYNSLGGADLTTPFGEQELVNSGKIF 120
QY 126 YQRYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLKPRAQPGQSSPKIDVWVISEA 185
Db 121 YQRYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLKPRAQPGQSSPKIDVWVISEA 180
QY 186 SSSNNTLDPGCTVPEDESADTVEANFTATVPFVPSIRQLENDLSGVTLTDTTEVTYLMDM 245
Db 181 SSSNNTLDPGCTVPEDESADTVEANFTATVPFVPSIRQLENDLSGVTLTDTTEVTYLMDM 240
QY 246 CSFDTISTSTVDTKLSPFCDLTFHDEWINYDLSLKKYKGAGNPLGPTQGVGYANEL 305
Db 241 CSFDTISTSTVDTKLSPFCDLTFHDEWINYDLSLKKYKGAGNPLGPTQGVGYANEL 300
QY 306 IARLTHSPVHDDTSNHTLSDSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 365
Db 301 IARLTHSPVHDDTSNHTLSDSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 360
QY 366 TTVENITQDGFSSAWTVPFASRLYVENMQCOAEQELVRLVNDRVVPLHGPCVDALGR 425
Db 361 TTVENITQDGFSSAWTVPFASRLYVENMQCOAEQELVRLVNDRVVPLHGPCVDALGR 420
QY 426 CTRDSFVRGLSFARSGGDWAECA 449
Db 421 CTRDSFVRGLSFARSGGDWAECA 444
RESULT 13
US-09-684-855-105
; Sequence 105, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 105
; LENGTH: 441
; TYPE: PR
; ORGANISM: A. niger NRRL3135
; US-09-684-855-105

Query Match          98.4%; Score 2321; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.7e-231;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NQSSCDTVDOGYQCFSTSHLWGQYAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARY 68
Db 1 NQSSCDTVDOGYQCFSTSHLWGQYAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARY 60

Qy 69 PTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNSIGADDLTPFGQEQLVNSGIKFYOR 128
Db 61 PTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNSIGADDLTPFGQEQLVNSGIKFYOR 120

Qy 129 YESLTRNIVPFISSGSSSRVIAAGKKEIEGFQSTKLKDPRAQPGQSSPKIDVWVISEASS 188
Db 121 YESLTRNIVPFISSGSSSRVIAAGKKEIEGFQSTKLKDPRAQPGQSSPKIDVWVISEASS 180

Qy 189 NNTLDPGCTCTVFDESELADTVEANFTATFVPSIRQRLNDLSGVTLTDTTEVTYLMDCSF 248
Db 181 NNTLDPGCTCTVFDESELADTVEANFTATFVPSIRQRLNDLSGVTLTDTTEVTYLMDCSF 240

Qy 249 DTISTSTVDTKLSPFCDLFTHDEWINDYLSLKKYKHGAGNPLGPTQGVGYNELIAR 308
Db 241 DTISTSTVDTKLSPFCDLFTHDEWINDYLSLKKYKHGAGNPLGPTQGVGYNELIAR 300

Qy 309 LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTV 368
Db 301 LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTV 360

Qy 369 ENITQDGFSSAMTVFPASRLYVEMMQCAEQEPLVRVNDRVVPLHGPCFVDALGRCTR 428
Db 361 ENITQDGFSSAMTVFPASRLYVEMMQCAEQEPLVRVNDRVVPLHGPCFVDALGRCTR 420

Qy 429 DSFVRLGSLFARSGGDWAECEFA 449
Db 421 DSFVRLGSLFARSGGDWAECEFA 441

RESULT 14
US-09-684-855-127
; Sequence 127, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 127
; LENGTH: 441
; TYPE: PR
; ORGANISM: A. niger NRRL3135
; US-09-684-855-127

Query Match          98.4%; Score 2321; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.7e-231;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NQSSCDTVDOGYQCFSTSHLWGQYAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARY 68
Db 1 NQSSCDTVDOGYQCFSTSHLWGQYAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARY 60

Qy 69 PTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNSIGADDLTPFGQEQLVNSGIKFYOR 128
Db 61 PTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNSIGADDLTPFGQEQLVNSGIKFYOR 120

Qy 129 YESLTRNIVPFISSGSSSRVIAAGKKEIEGFQSTKLKDPRAQPGQSSPKIDVWVISEASS 188
Db 121 YESLTRNIVPFISSGSSSRVIAAGKKEIEGFQSTKLKDPRAQPGQSSPKIDVWVISEASS 180

Qy 189 NNTLDPGCTCTVFDESELADTVEANFTATFVPSIRQRLNDLSGVTLTDTTEVTYLMDCSF 248
Db 181 NNTLDPGCTCTVFDESELADTVEANFTATFVPSIRQRLNDLSGVTLTDTTEVTYLMDCSF 240

Qy 249 DTISTSTVDTKLSPFCDLFTHDEWINDYLSLKKYKHGAGNPLGPTQGVGYNELIAR 308
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Qy 309 LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTV 368
Db 301 LTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTV 360

Qy 369 ENITQDGFSSAMTVFPASRLYVEMMQCAEQEPLVRVNDRVVPLHGPCFVDALGRCTR 428
Db 361 ENITQDGFSSAMTVFPASRLYVEMMQCAEQEPLVRVNDRVVPLHGPCFVDALGRCTR 420

Qy 429 DSFVRLGSLFARSGGDWAECEFA 449
Db 421 DSFVRLGSLFARSGGDWAECEFA 441

RESULT 15
US-09-684-855-150
; Sequence 150, Application US/09684855
; Patent No. 6599735
; GENERAL INFORMATION:
; APPLICANT: F. Hoffmann-La Roche AG
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS
; FILE REFERENCE: C38435/111692
; CURRENT APPLICATION NUMBER: US/09/684,855
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: EP 00121663.9
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: EP 99120289.6
; PRIOR FILING DATE: 1999-10-11
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 150
; LENGTH: 441
; TYPE: PR
; ORGANISM: A. niger NRRL3135
; US-09-684-855-150

Query Match          98.4%; Score 2321; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.7e-231;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NQSSCDTVDOGYQCFSTSHLWGQYAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARY 68
Db 1 NQSSCDTVDOGYQCFSTSHLWGQYAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARY 60

Qy 69 PTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNSIGADDLTPFGQEQLVNSGIKFYOR 128
Db 61 PTDSKGGKYSALIEEIQONATTFDGKYAFILKTYNSIGADDLTPFGQEQLVNSGIKFYOR 120

Qy 129 YESLTRNIVPFISSGSSSRVIAAGKKEIEGFQSTKLKDPRAQPGQSSPKIDVWVISEASS 188
Db 121 YESLTRNIVPFISSGSSSRVIAAGKKEIEGFQSTKLKDPRAQPGQSSPKIDVWVISEASS 180

Qy 189 NNTLDPGCTCTVFDESELADTVEANFTATFVPSIRQRLNDLSGVTLTDTTEVTYLMDCSF 248
Db 181 NNTLDPGCTCTVFDESELADTVEANFTATFVPSIRQRLNDLSGVTLTDTTEVTYLMDCSF 240

Qy 249 DTISTSTVDTKLSPFCDLFTHDEWINDYLSLKKYKHGAGNPLGPTQGVGYNELIAR 308
Db 241 DTISTSTVDTKLSPFCDLFTHDEWINDYLSLKKYKHGAGNPLGPTQGVGYNELIAR 300
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Db	241	DTISTVTDTKLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIAR	300
Qy	309	LTHSEVHDDTSSNHTLDSSPATEPLNSTLYADFSDNGIISILFALGLYNGTKPLSTTTV	368
Db	301	LTHSEVHDDTSSNHTLDSSPATEPLNSTLYADFSDNGIISILFALGLYNGTKPLSTTTV	360
Qy	369	ENITQTDGFSSAWTVPFASRLYVENMMQCAEQEPLVRVLVNDRVVPLHGCPCVDALGRCTR	428
Db	361	ENITQTDGFSSAWTVPFASRLYVENMMQCAEQEPLVRVLVNDRVVPLHGCPCVDALGRCTR	420
Qy	429	DSFVRGLSFARSGGDWAECPA	449
Db	421	DSFVRGLSFARSGGDWAECPA	441

Search completed: October 24, 2004, 13:00:11
Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 24, 2004, 12:58:14 ; Search time 1060 Seconds
(without alignments)
137.139 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

Sequence: 1 MLAVPASRNQSCSDTDQGY.....SFVRGLSPARSGDWAECFA 449

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1364641 seqs, 323758627 residues

Total number of hits satisfying chosen parameters: 1364641

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2353	99.8	467	14	US-10-079-709-32
2	2353	99.8	467	14	US-10-229-358-5
3	2353	99.8	467	16	US-10-662-914-2
4	2350	99.7	467	16	US-10-662-914-22
5	2350	99.7	467	16	US-10-662-914-28
6	2349	99.6	467	16	US-10-662-914-8
7	2349	99.6	467	16	US-10-662-914-18
8	2349	99.6	467	16	US-10-662-914-20
9	2349	99.6	467	16	US-10-662-914-24
10	2349	99.6	467	16	US-10-662-914-34
11	2347	99.5	467	16	US-10-662-914-6
12	2347	99.5	467	16	US-10-662-914-16
13	2347	99.5	467	16	US-10-662-914-30

14	2347	99.5	467	16	US-10-662-914-32
15	2346	99.5	467	16	US-10-662-914-12
16	2346	99.5	467	16	US-10-662-914-26
17	2346	99.5	467	16	US-10-662-914-40
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19	2345	99.4	467	16	US-10-662-914-42
20	2343	99.4	467	16	US-10-662-914-38
21	2343	99.4	467	16	US-10-662-914-69
22	2342	99.3	467	15	US-10-662-914-44
23	2341	99.3	467	13	US-10-083-452-11
24	2341	99.3	467	16	US-10-662-914-50
25	2341	99.3	467	16	US-10-662-914-52
26	2341	99.3	467	16	US-10-734-510-11
27	2340	99.2	467	16	US-10-662-914-54
28	2339	99.2	467	16	US-10-662-914-46
29	2339	99.2	467	16	US-10-662-914-48
30	2334	99.0	444	14	US-10-082-848-1
31	2334	99.0	444	16	US-10-776-104-1
32	2327	98.7	467	16	US-10-662-914-56
33	2321	98.4	441	14	US-10-442-538-105
34	2321	98.4	441	14	US-10-442-538-127
35	2321	98.4	441	14	US-10-442-538-150
36	2321	98.4	462	14	US-10-229-358-12
37	2288	97.0	441	14	US-10-442-538-104
38	2288	97.0	441	14	US-10-442-538-149
39	2278	96.6	467	9	US-09-929-060-3
40	2277	96.6	441	14	US-10-442-538-103
41	2277	96.6	441	14	US-10-442-538-126
42	2277	96.6	441	14	US-10-442-538-148
43	2255	95.6	443	9	US-09-929-060-1
44	2242	95.1	443	9	US-09-929-060-2
45	1990	84.4	410	14	US-10-229-358-11

ALIGNMENTS

RESULT 1

US-10-079-709-32
; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Seltin
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 02-FEB-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,510
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991

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; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-079-709-32

Query Match 99.8%; Score 2353; DB 14; Length 467;
Best Local Similarity 100.0%; Pred. No. 6.3e-208;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTQAQVL 61
Db 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTQAQVL 79
QY 62 SRHGARYPTDSKGYKSALIEEIQONATTFDGKYAFILKTYNYSIGADDLTPFGQEQLVNS 121
Db 80 SRHGARYPTDSKGYKSALIEEIQONATTFDGKYAFILKTYNYSIGADDLTPFGQEQLVNS 139
QY 122 GIKFYQRYESLIRNIVPFISSGSSRVIASGKFIQFQSTKLKDPRAQPGQSSPKIDVV 181
Db 140 GIKFYQRYESLIRNIVPFISSGSSRVIASGKFIQFQSTKLKDPRAQPGQSSPKIDVV 199
QY 182 ISEASSNNLTDPGTCVTFEDELADTVEANFTATFVPSIRQLENDLSGVTLTDTEVTY 241
Db 200 ISEASSNNLTDPGTCVTFEDELADTVEANFTATFVPSIRQLENDLSGVTLTDTEVTY 259
QY 242 LDMCSPDITISTVDTKLSPPCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGY 301
Db 260 LDMCSPDITISTVDTKLSPPCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHONGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHONGIISILFALGLYNGTK 379
QY 362 PLSTTTVENTITQDGFSSAWTVFFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPCVD 421
Db 380 PLSTTTVENTITQDGFSSAWTVFFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPCVD 439
QY 422 ALGCRTRDSFVRGLSFARSGGDWAECPA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECPA 467

RESULT 2
US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.O.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; FILE REFERENCE: GC596-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger

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US-10-229-358-5

Query Match 99.8%; Score 2353; DB 14; Length 467;
Best Local Similarity 100.0%; Pred. No. 6.3e-208;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTQAQVL 61
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QY 62 SRHGARYPTDSKGYKSALIEEIQONATTFDGKYAFILKTYNYSIGADDLTPFGQEQLVNS 121
Db 80 SRHGARYPTDSKGYKSALIEEIQONATTFDGKYAFILKTYNYSIGADDLTPFGQEQLVNS 139
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Db 140 GIKFYQRYESLIRNIVPFISSGSSRVIASGKFIQFQSTKLKDPRAQPGQSSPKIDVV 199
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QY 242 LDMCSPDITISTVDTKLSPPCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGY 301
Db 260 LDMCSPDITISTVDTKLSPPCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHONGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHONGIISILFALGLYNGTK 379
QY 362 PLSTTTVENTITQDGFSSAWTVFFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPCVD 421
Db 380 PLSTTTVENTITQDGFSSAWTVFFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPCVD 439
QY 422 ALGCRTRDSFVRGLSFARSGGDWAECPA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECPA 467

RESULT 3
US-10-662-914-2
; Sequence 2, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J.
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-662-914-2

Query Match 99.8%; Score 2353; DB 16; Length 467;
Best Local Similarity 100.0%; Pred. No. 6.3e-208;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTQAQVL 61
Db 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTQAQVL 79
QY 62 SRHGARYPTDSKGYKSALIEEIQONATTFDGKYAFILKTYNYSIGADDLTPFGQEQLVNS 121
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Db 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467

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US-10-662-914-22
; Sequence 22, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 22
; LENGTH: 467
; TYPE: PRF
; ORGANISM: Aspergillus niger
US-10-662-914-22

Query Match 99.7%; Score 2350; DB 16; Length 467;
Best Local Similarity 99.8%; Pred. No. 1.2e-207;
Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWQYAPFFSLANESVISPEVPACGRVTFQAQVL 79
Qy 62 SRHGARYPTDSKGYKYSALIEIQONATTFDGKAFKTYNYSLGADDLTPFGQELVNS 121
Db 80 SRHGARYPTDSKGYKYSALIEIQONATTFDGKAFKTYNYSLGADDLTPFGQELVNS 139
Qy 122 GIKFYQYESLTRNIVPIRSGSSRVIASGKKEGQSTKLKDPRAQPGQSSPKIDVV 181
Db 140 GIKFYQYESLTRNIVPIRSGSSRVIASGKKEGQSTKLKDPRAQPGQSSPKIDVV 199
Qy 182 ISEASSNNLTDPGCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDEVTY 241
Db 200 ISEASSNNLTDPGCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDEVTY 259
Qy 242 LMDCSFDTISTSTVDTKLSPFCDLTHDEWINDYLSLKKYGHGAGNPLGPTQGVY 301
Db 260 LMDCSFDTISTSTVDTKLSPFCDLTHDEWINDYLSLKKYGHGAGNPLGPTQGVY 319
Qy 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLNDRVVPPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLNDRVVPPLHGCPVD 439
Qy 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467

320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLNDRVVPPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLNDRVVPPLHGCPVD 439
Qy 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 5
US-10-662-914-28
; Sequence 28, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 28
; LENGTH: 467
; TYPE: PRF
; ORGANISM: Aspergillus niger
US-10-662-914-28

Query Match 99.7%; Score 2350; DB 16; Length 467;
Best Local Similarity 99.8%; Pred. No. 1.2e-207;
Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWQYAPFFSLANESVISPEVPACGRVTFQAQVL 61
Db 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWQYAPFFSLANESVISPEVPACGRVTFQAQVL 79
Qy 62 SRHGARYPTDSKGYKYSALIEIQONATTFDGKAFKTYNYSLGADDLTPFGQELVNS 121
Db 80 SRHGARYPTDSKGYKYSALIEIQONATTFDGKAFKTYNYSLGADDLTPFGQELVNS 139
Qy 122 GIKFYQYESLTRNIVPIRSGSSRVIASGKKEGQSTKLKDPRAQPGQSSPKIDVV 181
Db 140 GIKFYQYESLTRNIVPIRSGSSRVIASGKKEGQSTKLKDPRAQPGQSSPKIDVV 199
Qy 182 ISEASSNNLTDPGCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDEVTY 241
Db 200 ISEASSNNLTDPGCTVFEDSELADTVEANFTATFVPSIRQRLNDLSGVTLTDEVTY 259
Qy 242 LMDCSFDTISTSTVDTKLSPFCDLTHDEWINDYLSLKKYGHGAGNPLGPTQGVY 301
Db 260 LMDCSFDTISTSTVDTKLSPFCDLTHDEWINDYLSLKKYGHGAGNPLGPTQGVY 319
Qy 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLNDRVVPPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLNDRVVPPLHGCPVD 439
Qy 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 6
US-10-662-914-8
; Sequence 8, Application US/10662914

```
; Publication No. US2004012684A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; PRIOR FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 467
; TYPE: PR
; ORGANISM: Aspergillus niger
US-10-662-914-8

Query Match          99.6%; Score 2349; DB 16; Length 467;
Best Local Similarity 99.8%; Pred. No. 1.5e-207;
Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQGYCCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTTAQVL 61
D 20 LAVPASRNQSSCDTVDQGYCCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTTAQVL 79
QY 62 SRHGARYPTDSKGKYSALIEEQONATTFDGKYAFKTYNYSLGADDLTPFGEQELVNS 121
D 80 SRHGARYPTDSKGKYSALIEEQONATTFDGKYAFKTYNYSLGADDLTPFGEQELVNS 139
QY 122 GIKFYQRYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVV 181
D 140 GIKFYQRYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVV 199
QY 182 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATVPFSIRQBLENDLSGVTITDTEVTY 241
D 200 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATVPFSIRQBLENDLSGVTITDTEVTY 259
QY 242 LMDMCSFDTISTSTVDTKLSPPCDLFTHDEWINYDYLQSLKYYKGAGNPLGPTQGVY 301
D 260 LMDMCSFDTISTSTVDTKLSPPCDLFTHDEWINYDYLQSLKYYKGAGNPLGPTQGVY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 361
D 320 ANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGSSAWTPPFASRLYVEMMQCOAEPLVRLVNDRVVPLHGCPCVD 421
D 380 PLSTTTVENITQTDGSSAWTPPFASRLYVEMMQCOAEPLVRLVNDRVVPLHGCPCVD 439
QY 422 ALGRCTRDSFVRGLSPARSGGDWAECA 449
D 440 ALGRCTRDSFVRGLSPARSGGDWAECA 467

RESULT 8
US-10-662-914-20
; Sequence 20, Application US/10662914
; Publication No. US2004012684A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 467
; TYPE: PR
; ORGANISM: Aspergillus niger
US-10-662-914-20

Query Match          99.6%; Score 2349; DB 16; Length 467;
Best Local Similarity 99.8%; Pred. No. 1.5e-207;
Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQGYCCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTTAQVL 61
D 20 LAVPASRNQSSCDTVDQGYCCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTTAQVL 79
QY 62 SRHGARYPTDSKGKYSALIEEQONATTFDGKYAFKTYNYSLGADDLTPFGEQELVNS 121
D 80 SRHGARYPTDSKGKYSALIEEQONATTFDGKYAFKTYNYSLGADDLTPFGEQELVNS 139
QY 122 GIKFYQRYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVV 181
D 140 GIKFYQRYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVV 199
QY 182 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATVPFSIRQBLENDLSGVTITDTEVTY 241
D 200 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATVPFSIRQBLENDLSGVTITDTEVTY 259
QY 242 LMDMCSFDTISTSTVDTKLSPPCDLFTHDEWINYDYLQSLKYYKGAGNPLGPTQGVY 301
D 260 LMDMCSFDTISTSTVDTKLSPPCDLFTHDEWINYDYLQSLKYYKGAGNPLGPTQGVY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 361
D 320 ANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDGSSAWTPPFASRLYVEMMQCOAEPLVRLVNDRVVPLHGCPCVD 421
D 380 PLSTTTVENITQTDGSSAWTPPFASRLYVEMMQCOAEPLVRLVNDRVVPLHGCPCVD 439
QY 422 ALGRCTRDSFVRGLSPARSGGDWAECA 449
D 440 ALGRCTRDSFVRGLSPARSGGDWAECA 467

RESULT 7
US-10-662-914-18
; Sequence 18, Application US/10662914
; Publication No. US2004012684A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
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Db 80 SRHGARYPTDSKGYKYSALIEBIOQNATTFDGYAF.LKTYNSLGADDLTPFGQELVNS 139
Qy 122 GIKFYQRYESLTRNIVPIRSGSSRVASGKKIEGFQSTKLDPPRAQPGQSSPKIDV 181
Db 140 GIKFYQRYESLTRNIVPIRSGSSRVASGKKIEGFQSTKLDPPRAQPGQSSPKIDV 199
Qy 182 ISEASSNNLTDPGCTCTVFESLADTVEANFTATFVPSIRQLENDLSGVTLDTEVTY 241
Db 200 ISEASSNNLTDPGCTCTVFESLADTVEANFTATFVPSIRQLENDLSGVTLDTEVTY 259
Qy 242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYGHGAGNPLGPTQGVY 301
Db 260 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYGHGAGNPLGPTQGVY 319
Qy 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 439
Qy 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467
RESULT 9
US-10-662-914-24
; Sequence 24, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; PRIOR FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 24
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-662-914-24
Query Match 99.6%; Score 2349; DB 16; Length 467;
Best Local Similarity 99.8%; Pred. No. 1.5e-207;
Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 LAVPASRQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVL 61
Db 20 LAVPASRQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVL 79
Qy 62 SRHGARYPTDSKGYKYSALIEBIOQNATTFDGYAF.LKTYNSLGADDLTPFGQELVNS 121
Db 80 SRHGARYPTDSKGYKYSALIEBIOQNATTFDGYAF.LKTYNSLGADDLTPFGQELVNS 139
Qy 122 GIKFYQRYESLTRNIVPIRSGSSRVASGKKIEGFQSTKLDPPRAQPGQSSPKIDV 181
Db 140 GIKFYQRYESLTRNIVPIRSGSSRVASGKKIEGFQSTKLDPPRAQPGQSSPKIDV 199
Qy 182 ISEASSNNLTDPGCTCTVFESLADTVEANFTATFVPSIRQLENDLSGVTLDTEVTY 241
Db 200 ISEASSNNLTDPGCTCTVFESLADTVEANFTATFVPSIRQLENDLSGVTLDTEVTY 259
Qy 242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYGHGAGNPLGPTQGVY 301
Db 260 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYGHGAGNPLGPTQGVY 319
Qy 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 439
Qy 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467

Qy 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 439
Qy 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467
RESULT 10
US-10-662-914-34
; Sequence 34, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; PRIOR FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 34
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-662-914-34
Query Match 99.6%; Score 2349; DB 16; Length 467;
Best Local Similarity 99.8%; Pred. No. 1.5e-207;
Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 LAVPASRQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVL 61
Db 20 LAVPASRQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVL 79
Qy 62 SRHGARYPTDSKGYKYSALIEBIOQNATTFDGYAF.LKTYNSLGADDLTPFGQELVNS 121
Db 80 SRHGARYPTDSKGYKYSALIEBIOQNATTFDGYAF.LKTYNSLGADDLTPFGQELVNS 139
Qy 122 GIKFYQRYESLTRNIVPIRSGSSRVASGKKIEGFQSTKLDPPRAQPGQSSPKIDV 181
Db 140 GIKFYQRYESLTRNIVPIRSGSSRVASGKKIEGFQSTKLDPPRAQPGQSSPKIDV 199
Qy 182 ISEASSNNLTDPGCTCTVFESLADTVEANFTATFVPSIRQLENDLSGVTLDTEVTY 241
Db 200 ISEASSNNLTDPGCTCTVFESLADTVEANFTATFVPSIRQLENDLSGVTLDTEVTY 259
Qy 242 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYGHGAGNPLGPTQGVY 301
Db 260 LMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYGHGAGNPLGPTQGVY 319
Qy 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy 362 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 421
Db 380 PLSTTTVENITQTDGFSASNTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 439
Qy 422 ALGCRTRDSFVRGLSFARSGGDWAECEFA 449
Db 440 ALGCRTRDSFVRGLSFARSGGDWAECEFA 467

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RESULT 11
US-10-662-914-6
; Sequence 6, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-662-914-6

Query Match          99.5%; Score 2347; DB 16; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.3e-207;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 LAVPASRNQSSCDTVDQGYCFCSETSHLMGQYAPFFSLANESVISPEVPAGCRVTTAQVL 61
    |||||
Db  20 LAVPASRNQSSCDTVDQGYCFCSETSHLMGQYAPFFSLANESVISPEVPAGCRVTTAQVL 79
    |||||
QY  62 SRHGARYPTDSKGGKYSALIEETQQNATTFDGKYAFKTYNYSGLGADDTTPFGQEQLVNS 121
    |||||
Db  80 SRHGARYPTDSKGGKYSALIEETQQNATTFDGKYAFKTYNYSGLGADDTTPFGQEQLVNS 139
    |||||
QY  122 GIKFYQRYESLRTNIVPFRSSGSSRVIASGKKFIEGFQSTKLDKPRAGQGSSPKIDVV 181
    |||||
Db  140 GIKFYQRYESLRTNIVPFRSSGSSRVIASGKKFIEGFQSTKLDKPRAGQGSSPKIDVV 199
    |||||
QY  182 ISEASSNNLTDPGTCCTVFEDSELADTVANFTATVPFSIRQRENDLSGVTLTDTTEVY 241
    |||||
Db  200 ISEASSNNLTDPGTCCTVFEDSELADTVANFTATVPFSIRQRENDLSGVTLTDTTEVY 259
    |||||
QY  242 LMDMCSFDITSTVDTKLSPPCDLFTHDEWINYDLSLKKYYGHGAGNPLGPTQGVGY 301
    |||||
Db  260 LMDMCSFDITSTVDTKLSPPCDLFTHDEWINYDLSLKKYYGHGAGNPLGPTQGVGY 319
    |||||
QY  302 ANELIARLTHSPVHDDTSSNHTLDSSPATPPLNSTLYADFSHDNGIISILFALGLYNGTK 361
    |||||
Db  320 ANELIARLTHSPVHDDTSSNHTLDSSPATPPLNSTLYADFSHDNGIISILFALGLYNGTK 379
    |||||
QY  362 PLSTTTVENITQDGFSSAWTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPCVD 421
    |||||
Db  380 PLSTTTVENITQDGFSSAWTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPCVD 439
    |||||
QY  422 ALGRCTRDSFVRGLSPARSGGDWAECEFA 449
    |||||
Db  440 ALGRCTRDSFVRGLSPARSGGDWAECEFA 467
    |||||

RESULT 13
US-10-662-914-30
; Sequence 30, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-662-914-30

Query Match          99.5%; Score 2347; DB 16; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.3e-207;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 LAVPASRNQSSCDTVDQGYCFCSETSHLMGQYAPFFSLANESVISPEVPAGCRVTTAQVL 61
    |||||
Db  20 LAVPASRNQSSCDTVDQGYCFCSETSHLMGQYAPFFSLANESVISPEVPAGCRVTTAQVL 79
    |||||
QY  62 SRHGARYPTDSKGGKYSALIEETQQNATTFDGKYAFKTYNYSGLGADDTTPFGQEQLVNS 121
    |||||
Db  80 SRHGARYPTDSKGGKYSALIEETQQNATTFDGKYAFKTYNYSGLGADDTTPFGQEQLVNS 139
    |||||
QY  122 GIKFYQRYESLRTNIVPFRSSGSSRVIASGKKFIEGFQSTKLDKPRAGQGSSPKIDVV 181
    |||||
Db  140 GIKFYQRYESLRTNIVPFRSSGSSRVIASGKKFIEGFQSTKLDKPRAGQGSSPKIDVV 199
    |||||
QY  182 ISEASSNNLTDPGTCCTVFEDSELADTVANFTATVPFSIRQRENDLSGVTLTDTTEVY 241
    |||||
Db  200 ISEASSNNLTDPGTCCTVFEDSELADTVANFTATVPFSIRQRENDLSGVTLTDTTEVY 259
    |||||
QY  242 LMDMCSFDITSTVDTKLSPPCDLFTHDEWINYDLSLKKYYGHGAGNPLGPTQGVGY 301
    |||||
Db  260 LMDMCSFDITSTVDTKLSPPCDLFTHDEWINYDLSLKKYYGHGAGNPLGPTQGVGY 319
    |||||
QY  302 ANELIARLTHSPVHDDTSSNHTLDSSPATPPLNSTLYADFSHDNGIISILFALGLYNGTK 361
    |||||
Db  320 ANELIARLTHSPVHDDTSSNHTLDSSPATPPLNSTLYADFSHDNGIISILFALGLYNGTK 379
    |||||
QY  362 PLSTTTVENITQDGFSSAWTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPCVD 421
    |||||
Db  380 PLSTTTVENITQDGFSSAWTVPFASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPCVD 439
    |||||
QY  422 ALGRCTRDSFVRGLSPARSGGDWAECEFA 449
    |||||
Db  440 ALGRCTRDSFVRGLSPARSGGDWAECEFA 467
    |||||

RESULT 12
US-10-662-914-16
; Sequence 16, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
```

Db 20 LAVPASRNQSSCDTVDQGYQCFSFSETSHLWGOYAPFFSLANESVISPEVPAGCRVTFQAQVL 79
Qy 62 SRHGARYPTDSKGGKYSALIEIEIQONATTFDQKYAFLKTYNYSIGADDLTPFGQELVNS 121
Db 80 SRHGARYPTDSKGGKYSALIEIEIQONATTFDQKYAFLKTYNYSIGADDLTPFGQELVNS 139
Qy 122 GIKFYQRYESLTRNIVPPIRSGSSSRVSIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDV 181
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RESULT 14

US-10-662-914-32
; Sequence 32, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H. J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES

; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-662-914-32

Query Match 99.5%; Score 2347; DB 16; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.3e-207;
Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LAVPASRNQSSCDTVDQGYQCFSFSETSHLWGOYAPFFSLANESVISPEVPAGCRVTFQAQVL 61
Db 20 LAVPASRNQSSCDTVDQGYQCFSFSETSHLWGOYAPFFSLANESVISPEVPAGCRVTFQAQVL 79
Qy 62 SRHGARYPTDSKGGKYSALIEIEIQONATTFDQKYAFLKTYNYSIGADDLTPFGQELVNS 121
Db 80 SRHGARYPTDSKGGKYSALIEIEIQONATTFDQKYAFLKTYNYSIGADDLTPFGQELVNS 139
Qy 122 GIKFYQRYESLTRNIVPPIRSGSSSRVSIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDV 181
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Qy 242 LMDMCSFDITSTSTVDTKLSPFCDLFTHDEWINYDYLQSLKYYGHGAGNPLGPTQGVGY 301
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RESULT 15

US-10-662-914-12
; Sequence 12, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H. J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES

; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-662-914-12

Query Match 99.5%; Score 2346; DB 16; Length 467;
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Matches 447; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 380 PLSTTTVENITQTDFSSAWTVPFASRLYVEMMOCQAEQEPFLVRVLNDRVVLHGCPVD 439
Qy 422 ALGRCTRDSFVRGLSFARSGGDWAECEFA 449

Db 440 ALGRCTRDSEVRGLSFARSGDWAECEFA 467

Search completed: October 24, 2004, 13:24:29
Job time : 1062 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 13:00:14 ; Search time 7951 Seconds
(without alignments)
2670.491 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODEB=LOCAL
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2353	99.8	1404	6 AI9452	AI9452 phytase cdn
3	2353	99.8	1404	6 I13430	I13430 Sequence 33
4	2353	99.8	1404	6 I33881	I33881 Sequence 19

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5 2353 99.8 1404 6 AR195149 Sequence
6 2353 99.8 2000 8 ANPHYAG
7 2353 99.8 2665 8 ASNPHTASE
8 2353 99.8 6756 6 AI9451
9 2353 99.8 6756 6 I13429
10 2353 99.8 6756 6 AR195148
11 2324 98.6 1525 8 AY426977
12 2313 98.1 1528 8 AF218813
13 2309 97.9 2363 6 AR018076
14 2309 97.9 2363 6 AR051916
15 2309 97.9 2379 8 AR053934
16 2309 97.9 2379 8 ASNPHTAS
17 2309 97.4 1347 12 AF547224
18 2296 97.4 1434 12 AY182953
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ALIGNMENTS

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DEFINITION 1350 bp mRNA linear SYN 18-OCT-2000
ACCESSION AF295325
VERSION AF295325.1 GI:10732782
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 1350)
AUTHORS Yang,L., Chen,Z., Bei,J., Liao,L. and Wang,X.
TITLE Synthetic sequence of phytase gene for expression in Pichia
pastoris
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1350)
AUTHORS Chen,Z.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-2000) Animal Science Institute, Guangdong Academy
of Agricultural Sciences, Guangzhou, Guangdong 510640, China
REFERENCE 3 (bases 1 to 1350)
AUTHORS Yang,L., Bei,J., Liao,L. and Wang,X.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-2000) Biopharmaceutical Center, Zhongshan
University, Guangzhou, Guangdong 510275, China
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Alignment Scores:
Pred. No.: 7,02e-187 Length: 1404
Score: 2353.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.79% Indels: 0
DB: 6 Gaps: 0

US-10-089-364-4 (1-449) x A19452 (1-1404)

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Qy 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
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Qy 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
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VERSION I13430.1 GI:910771
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1404)
AUTHORS Van Gorkom, R.F.M., Van Hartingsveldt, W., Van Paridon, P.A.,
Veenstra, A.E., Luiten, R.G.M. and Sellen, G.C.M.
TITLE Cloning and expression of phytase from aspergillus
JOURNAL Patent: US 5436156-A 33 25-JUL-1995;
FEATURES Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.: 7,02e-187 Length: 1404
Score: 2353.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.79% Indels: 0
DB: 6 Gaps: 0

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QY 22 CysPheSerGluThrSerHisLeuTyrGlnTyrAlaProPhePheSerLeuAlaAsn 41
Db 118 TGCTTCTCCGAGACTTCGATCTTCCTGGGTCAATACGACCGCTTCCTCTGGCAAC 177
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QY 442 GlyAspTrpAlaGluCysPheAla 449
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VERSION
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KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
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REFERENCE
1 (bases 1 to 1404)
AUTHORS
Van Ooijen,A.J.J., Rietveld,K., Hoekema,A., Pen,J., Sijmons,P.C.
and Verwoerd,T.C.
TITLE
Expression of phytase in plants
JOURNAL
Patent: US 5593963-A 19 14-JAN-1997;
FEATURES
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Query Match: 99.79% Indels: 0
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DEFINITION Sequence 33 from patent US 6350602.
ACCESSION AR195149
VERSION AR195149.1 GI:20244586
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1404)
AUTHORS Van Gorcom,R.F.M., Van Hartingsveldt,W., Van Paridon,P.Andreas.,
Veenstra,A.Eveline., Luiten,R.G.M. and Seiten,G.C.M.
TITLE Cloning and expression of phytase from aspergillus
JOURNAL Patent: US 6350602-A 33 26-FEB-2002;
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 1 (bases 1 to 2000)
 van Hartingsveldt, W., Van Zeijl, C.M.J., Harteveld, M.G., Gouka, R.J.,
 Suykerbuyk, M.E.G., Luiten, R.G.M., Van Paridon, P.A., Selden, G.C.M.,
 Veenstra, A.E., Van Gorcom, R.F.M. and Van Den Hondel, C.A.M.J.
 Cloning, molecular characterization and overexpression of the
 phytase gene (phyA) of Aspergillus niger
 Gene (1992) In press
 2 (bases 1 to 2000)
 van Hartingsveldt, W.
 Direct Submission
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 Submitted (05-OCT-1992) Van Hartingsveldt W., TNO Medical
 Biological Laboratory, Lange Kleiweg 139, Rijswijk, the Netherlands
 Location/Qualifiers
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 REFERENCE 1 (bases 1 to 2665)
 Mullaney, E.J., Gibson, D.M. and Ullah, A.H.
 Positive identification of a lambda gt11 clone containing a region of fungal phytase gene by immunoprobe and sequence verification
 Appl. Microbiol. Biotechnol. 35 (5), 611-614 (1991)
 JOURNAL 92000601
 MEDLINE 1369340
 PUBMED 2 (bases 1 to 2665)
 REFERENCE Mullaney, E.J.
 TITLE Sequence of the Aspergillus niger (ficum) phytase gene
 JOURNAL Unpublished (1992)
 COMMENT Original source text: Aspergillus niger (library: EMBL 3; NRRL 3135) DNA.
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 Query Match: 99.79% Indels: 0
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 ACCESSION A19451
 VERSION A19451.1 GI:583193
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 SOURCE artificial construct
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 REFERENCE 1 (bases 1 to 6756)
 AUTHORS van Gorcom, R.F.M.; van Hartingsveldt, W.; van Paridon, P.A.;
 Veenstra, A.E.; Luiten, R.G.M. and Selten, G.C.M.
 TITLE Cloning and expression of microbial phytase
 JOURNAL Patent: EP 0420358-A 40 03-APR-1991;
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US-10-089-364-4 (1-449) x AI9451 (1-6756)

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DEFINITION Sequence 31 from patent US 5436156.
ACCESSION I13429
VERSION I13429.1 GI:910770
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6756)
AUTHORS Van Gorcom,R.F.M., Van Hartingsveldt,W., Van Paridon,P.A.,
Veenstra,A.E., Luiten,R.G.M. and Seiten,G.C.M.
TITLE Cloning and expression of phytase from aspergillus
JOURNAL Patent: US 5436156-A 31 25-JUL-1995;
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Score: 2353.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
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DEFINITION Sequence 31 from patent US 6350602..
ACCESSION AR195148
VERSION AR195148.1 GI:20244585
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 6756)
AUTHORS Van Gorcum,R.F.M., Van Hartingsveldt,W., Van Paridon,P.Andreas.,
Veenstra,A.Eveline., Luiten,R.G.M. and Selten,G.C.M.
TITLE Cloning and expression of phytase from aspergillus
JOURNAL Patent: US 6350602-A 31 26-FEB-2002;
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VERSION AY426977.1 GI:38018638
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PENG, Y. Y., Zhou, Z. Y., and Ma, L. P.
Cloning and characterization of phytase gene of Aspergillus niger
N14*
Unpublished
2 (bases 1 to 1525)
REFERENCE Peng, Y. Y., Zhou, Z. Y., and Ma, L. P.
AUTHORS Direct Submission
TITLE Submitted (01-OCT-2003) College of Animal Science & Technology,
JOURNAL Southwest Agricultural University, Tiansheng, Beibei, Chongqing
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Qy 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
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Qy 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
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Qy 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
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QY	222	ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr	241
Db	832	CGTCAACGCTGTGAGAACACCTGCTCGGGTGTCTCTCACACACACAGAGTACCTAC	891
QY	242	LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer	261
Db	892	CTCATGGACATGTGCTTCCTTCGACACTATCTCCACTAACACCGTCGACACCAAGCTGTC	951
QY	262	ProPheCysAspLeuPheThrHisAspGluTyrPheAsnTyrAspTyrLeuGlnSerLeu	281
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QY	302	AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn	321
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QY	382	ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu	401
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QY	402	ProLeuValArgValLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeu	421
Db	1372	CCGCTCGTCCGCTGTCTGT	1431
QY	422	AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly	441
Db	1432	GCTTTGGGAGATGTACCCGGATAGCTTTGTGAAGGGTTGAGCTTTGCTAGATCTGGG	1491
QY	442	GlyAspTrpAlaGluCysPheAla	449
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RESULT 12			
AF218813			
LOCUS			
DEFINITION			
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precursor, gene, complete cds.			
ACCESSION			
AF218813			
VERSION			
AF218813.1			
GI:6694940			
KEYWORDS			
Aspergillus niger			
ORGANISM			
Aspergillus niger			
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;			
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.			
REFERENCE			
1 (bases 1 to 1528)			
AUTHORS			
Hongning, W., Qi, W. and Jing, X.			
TITLE			
PCR, cloning and characterization of the phytase (phyA) gene of			
Aspergillus niger (China Strain)			
JOURNAL			
Unpublished			

REFERENCE	2 (bases 1 to 1528)	
AUTHORS	Hongning, W., Qi, W. and Jing, X.	
TITLE	Direct Submission	
JOURNAL	Submitted (24-DEC-1993) Aniaml Sci. & Tech. College, Sichuan Agricultural University, Ya an City, Sichuan Province 625014, P.R.China	
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	KLSFCDLDEHWINYDYLKKYIGHGAGNPLGPTQGVYANLRLARLHSPVHD	
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Best Local Similarity:	97.54%	Mismatches: 3
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QY	42	GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
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QY	102	AsnTyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
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QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
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QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
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QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
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QY 302 AlaAsnGluLeuIleAlaArgGluThrHisSerProValHisAspAspThrSerSerAsn 321
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AR018076

LOCUS

DEFINITION

Sequence 7 from patent US 5780292.

ACCESSION

AR018076

VERSION

AR018076.1

KEYWORDS

GI:3973679

SOURCE

Unknown.

ORGANISM

Unknown.

Unclassified.

1 (bases 1 to 2363)

REFERENCE

AUTHORS

Nevalainen,H.K.M., Palchoimo,M.T., Miettinen-Oinonen,A.S.K.,

Torkkeli,T.K., Cantrell,M., Piddington,C.S., Rambosek,J.A.,

Turunen,M.K. and Fagerstrom,R.B.

Production of phytate degrading enzymes in trichoderma

Patent: US 5780292-A 7 14-JUL-1998;

TITLE

JOURNAL

FEATURES

source

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Location/Qualifiers

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/mol_type="unassigned DNA"

ORIGIN

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Pred. No.: 6,55e-183

Score: 2309.00

Percent Similarity: 99.11%

Best Local Similarity: 97.32%

Query Match: 97.92%

Indels: 0

Gaps: 0

US-10-089-364-4 (1-449) x AR018076 (1-2363)

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QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41

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DEFINITION Sequence 7 from patent US 5830733.
ACCESSION AR051916
VERSION AR051916.1 GI:5975280
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2363)
AUTHORS Nevalainen,H.K.M., Paloheimo,M.T., Miettinen-Oinonen,A.S.K.,
Torkkeli,T.K., Cantrell,M., Piddington,C.S., Rambosek,J.A.,
Turunen,M.K., Fagerstrom,R.B. and Houston,C.S.
TITLE Nucleic acid molecules encoding phytylase and ph2.5 acid phosphatase
JOURNAL Patent: US 5830733-A 7 03-NOV-1998;
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Query Match: 97.92% Indels: 0
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 ACCESSION AR053934
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 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
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 1 (bases 1 to 2379)
 Nevalainen,H.K.M., Paloheimo,M.T., Fagerstrom,R.B.,
 Miettinen-Oinonen,A.S.K., Turunen,M.K., Rambousek,J.A.,
 Piddington,C.S., Houston,C.S. and Cantrell,M.A.
 Recombinant cells that express phytate degrading enzymes in desired
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 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
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 QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 DB 819 GAGGAGATCCAGCAGACGTGACCACCTTTGTATGAAAAATATGCCTTCTCTGAAGACATAC 878

QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
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 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
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 QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
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 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
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 QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
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Job time : 7987 secs

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 13:06:44 ; Search time 140 Seconds
(without alignments)
2279.601 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

Sequence: 1 MIAVPSNRQSCDVTDDGY.....SFVRLSFARSGDWAECFA 449

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Ygapop 10.0	Ygapext 0.5
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Delop 6.0	Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2353	99.8	1404	1	US-08-146-424-19
3	2353	99.8	1404	1	US-08-693-709-1
4	2353	99.8	1404	2	US-08-419-448-33
5	2353	99.8	1404	3	US-08-233-510-33
6	2353	99.8	6756	1	US-08-151-574-31
7	2353	99.8	6756	2	US-08-419-448-31
8	2353	99.8	6756	3	US-09-233-510-31
9	2309	97.9	2363	1	US-07-923-724-7
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11	2309	97.9	2379	2	US-08-374-652C-1
12	2278	96.6	1515	3	US-09-155-855-5

13	2278	96.6	1515	3	US-09-543-744-5	Sequence 5, Appli
14	2278	96.6	1515	4	US-09-929-060-5	Sequence 5, Appli
15	2255	95.6	1332	4	US-09-155-855-4	Sequence 4, Appli
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44	1534	65.1	1931	3	US-08-868-435-28	Sequence 28, Appl
45	1534	65.1	1931	3	US-08-744-231-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-08-151-574-33

; Sequence 33, Application US/08151574

; Patent No. 5436156

; GENERAL INFORMATION:

; APPLICANT: Robert F.M. Van Gorcom

; APPLICANT: Willem Van Hartingsveldt

; APPLICANT: Petrus A. Van Paridon

; APPLICANT: Annemarie E. Veenstra

; APPLICANT: Rudolf G.M. Luttin

; APPLICANT: Gerardus Seltin

; TITLE OF INVENTION: Cloning and Expression of Microbial

; TITLE OF INVENTION: Phytase

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morrison & Foerster

; STREET: 545 Middlefield Road, Suite 200

; CITY: Menlo Park

; STATE: California

; COUNTRY: USA

; ZIP: 94025-3471

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; SOFTWARE:

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/151,574

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/688,578

; FILING DATE: 24-MAY-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Murashige, Kate H.

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; REGISTRATION NUMBER: 29, 959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1404 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficum (Aspergillus niger)
; STRAIN: NRRL 3135
; US-08-151-574-33

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Score: 2353.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.79% Indels: 0
DB: 1 Gaps: 0

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RESULT 2
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; Sequence 19, Application US/08146424
; Patent No. 5593963
; GENERAL INFORMATION:
; APPLICANT: VAN OOLJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KRION
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/146,424
 FILING DATE: 02-NOV-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: KENNEDY, BILL
 REGISTRATION NUMBER: 33,407
 REFERENCE/DOCKET NUMBER: 44615-20011.24
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
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 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
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 LOCATION: 70
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 QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
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 QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 Db 1198 ACGTTCGCTTGTCTCGCTTGTACGTCCAGATGATGACAGTGTCTCAGCGCGAGCAGGAG 1257
 QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 Db 1258 CCGCTGTGCTCGTCTTGTGTTAATGATCGCGTGTCCGCTGCAATGGGTGCCGTTGAT 1317
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 1318 GCCTTGGGGAGATGATACCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGG 1377
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 Db 1378 GGTGATTGGGCGGAGTGTCTTGTCT 1401

RESULT 3

US-08-693-709-1
 ; Sequence 1, Application US/08693709
 ; Patent No. 5770413
 ; GENERAL INFORMATION:
 ; APPLICANT: VAN OIJEN, ALBERT J. J.
 ; APPLICANT: RIETVELD, KRIJN
 ; APPLICANT: HOEKEMA, ANDREAS
 ; APPLICANT: PEN JAN
 ; APPLICANT: SIMONS, PETER C.
 ; APPLICANT: VERWOERD, TEUNIS C.
 ; TITLE OF INVENTION: THE EXPRESSION OF PHVTASE
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 PAGE MILL ROAD
 ; CITY: Palo Alto
 ; STATE: CA

COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/693,709
 FILING DATE: 07-AUG-1996
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/146,424
 FILING DATE: 02-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Murashige, Kate H
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 24615-20011.10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-813-5600
 TELEFAX: 415-494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1404 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 1..1401
 OTHER INFORMATION:
 NAME/KEY: mat_peptide
 LOCATION: 70...1401
 OTHER INFORMATION:
 NAME/KEY: Signal Sequence
 LOCATION: 1..72
 OTHER INFORMATION:
 US-08-693-709-1

Alignment Scores:
 Pred. No.: 1,31e-275 Length: 1404
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservat: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 1 Gaps: 0

US-10-089-364-4 (1-449) x US-08-693-709-1 (1-1404)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 Db 58 CTGCGAGTCCCGCTCGAGAAATCAATCCAGTTGGCATACGGTCGATCGGGGTATCAA 117
 QY 22 CysPheSerGluThrSerHisLeuTyrGlnTyrAlaProPhePheSerLeuAlaAsn 41
 Db 118 TGTCTTCCGAGACTTCGATCTTTGGGTCAATACGACCGCTCTCTCTGGCAAC 177
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 178 GAATCGGTGATCTCCCTGAGTCCCGCTCGATGTCAGAGTCACTTTCTCGTTCAGTCTC 237
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerGlyLysLysTyrSerAlaLeuIle 81
 Db 238 TCCCGTTCATGAGCGCGGTATCCGACCGACTCCCAAGGGCAAGAAATCTCCGCTCTCAT 297
 QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 298 GAGGAGATCCAGCAGACGCGACCCACTTTCGACGGAAATATGCTTCTCCTGAAGACATAC 357
 QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluValAsnSer 121
 Db 358 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGAGAACAGGAGCTAGTCAACTCC 417

QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 418 GGCATCAAGTTCTACAGGGGTACGAATCGCTCAAGAGNACATCGTTCCATTCATCCGA 477
 QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 478 TCCTCTGGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCAGAGGCTTCAGAGC 537
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 Db 538 ACCAAGCTGAAGATCCTCGTCCCGAGCCCGCCCAATCGTCGCCCAAGATCGACGTGGTC 597
 QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 Db 598 ATTTCCGAGGCCAGCTCATCCAAACACTCTCGACCCAGGCACCTGCACTGCTTCGAA 657
 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 Db 658 GACAGCGAATTGGCCGATACCGTCGAAGCAATTTCCCGCCACGTCGTCCCTCCATT 717
 QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 Db 718 CGTCAACGCTCGAGAACGACCTGTCGGTGTGACTCTCAGACACACAGAGTGACCTAC 777
 QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
 Db 778 CTCATGACATGTGCTCCTTCGACACCATCTCCACGACCGCTCGACACCAAGCTGTCC 837
 QY 262 ProPheCysAspLeuPheThrHisAspGluTyrIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 838 CCCTTCTGTGACCTGTTCACCAATGGAATCACTACGACTACCTCCAGTCCCTTG 897
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 898 AAAAGTATTACGGCCATGTGTCAGATACCCGCTCGGCCGACCCAGGCGTCGCGTAC 957
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 958 GCTAACGAGCTCATCGCCGCTGACCCACTCGCTGTCCACGATGACACCAAGTCCAAC 1017
 QY 322 HisThrIleAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 Db 1018 CACACTTTGGACTCGAGCCCGGTACTCTTCCGCTCAACTCTACTCTCTACGGCGACTTT 1077
 QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 Db 1078 TCGCATGACAAACGGCATCATCTCCATCTCTTTGCTTTAGGTCTGTACACGCGACTAAG 1137
 QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
 Db 1138 CGCTATCTACACGACCGGTGGAGAAATATCACCGACAGATGATGATCTCGTCTGTGG 1197
 QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 Db 1198 ACGGTTCCGTTTCTCGCGTTTGTACGTGAGATGATGAGTGTACAGGCGAGACAGAG 1257
 QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 Db 1258 CCGCTGTCTCGTCTCTGGTTTATGATCGGTTGTCCCGCTGATCGGTGCGGTGAT 1317
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 1318 GCTTTGGGAGATGATCCCGGATAGCTTTGTGAGGGGTGAGCTTTGTAGATCTGGG 1377
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 Db 1378 GGTGATTGGCGGAGTGTCTTGCT 1401

RESULT 4

US-08-419-448-33

; Sequence 33, Application US/08419448

; Patent No. 5663533

GENERAL INFORMATION:
 APPLICANT: Robert F.M. Van Gorcom
 APPLICANT: Willem Van Hartingsveldt
 APPLICANT: Petrus A. Van Paridon
 APPLICANT: Annemarie E. Veenstra
 APPLICANT: Rudolf G.M. Luttin
 APPLICANT: Gerardus Selden
 TITLE OF INVENTION: Cloning and Expression of Microbial
 TITLE OF INVENTION: Phytase
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Mortison & Foerster
 STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20006-1888
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 SOFTWARE:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/419,448
 FILING DATE: 10-APR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Murashige, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 24615-20026.10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-887-1500
 INFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1404 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Aspergillus ficuum (Aspergillus niger)
 STRAIN: NRRL 3135
 US-08-419-448-33

Alignment Scores:
 Pred. No.: 1,31e-275 Length: 1404
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 2 Gaps: 0

US-10-089-364-4 (1-449) x US-08-419-448-33 (1-1404)

Qy 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 Db 58 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGCCGATACGGTCGATCAGGGGTATCAA 117
 Qy 22 CysPheSerGluThrSerHisLeuTyrGlnTyrAlaProPheSerLeuAlaAsn 41
 Db 118 TGCCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGCACCGTTCTTCTCTCGCAAC 177
 Qy 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 178 GAATCGGTCACTCCCTGAGTCCCGCGGATGCGAGTCACTTTCGCTCAGGTCTC 237
 Qy 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeu 81
 Db 238 TCCGTCATGGAGCGGGTATCCGACCGACTCCCAAGGCGAATAACTCCGCTCTCAT 297

Qy 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 298 GAGGAGATCCAGCAGAACCGGACCCTTTGACGGAAATATATCCCTTCTCTGAAGACATAC 357
 Qy 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
 Db 358 AACTACAGCTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGGAGTAGTCACTCC 417
 Qy 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 418 GGCATCAAGTTCTACACGGGTACGAATCGCTCACAAGGAACATCGTTCATTCATCCGA 477
 Qy 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 478 TCCTCTGGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCAGGGCTTCCAGAGC 537
 Qy 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 Db 538 ACCAAGCTGAAGGATCCTCGTCCAGCGCGGCAATCGTCCCAAGATCGACGTGGTC 597
 Qy 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 Db 598 ATTTCCGAGGCGCAGCTCATCCAAACACACTCTCGACCCAGGACCTGCATCTGTCTCGAA 657
 Qy 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 Db 658 GACAGCGAATGGCCGATACCGTCCGAAGCCAAATTCACCGCCACGTTCTGTCCTCCATT 717
 Qy 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 Db 718 CGTCAACGCTCGAGAACGACCTGCTCGGTGTGACTCTCACAGACACAGAAAGTGACCTAC 777
 Qy 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
 Db 778 CTCATGGACATGTGCTCCTTCGACACCATCTCCACACGACCGCTCGACACCAAGGTGCC 837
 Qy 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 838 CCCTTCTGTGACCTGTTCCACCATGACGAATGGATCAACTACGACTACTCCAGTCCCTTG 897
 Qy 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 898 AAAAAAGTATTACGGCCATGTGTCAGGTAAACCGCTCGGCCCGACCCAGGGGTGCGGTAC 957
 Qy 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 958 GCTAACGAGCTCATCGCCCGCTCGACCCACTCGCCTGTCCAAGATGACACCAAGTCCAAC 1017
 Qy 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 Db 1018 CACACTTGGACTCGAGCCCGGCTACCTTCCGCTCAACTCTACTCTCTACCGCGGACTTT 1077
 Qy 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 Db 1078 TCGCATGACAAACGCATCATCTCCATTCTCTTCTTTAGTCTGTACACGGGACTAAG 1137
 Qy 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
 Db 1138 CCGGTATCTACACGACCGGTGGAGATATCACCCAGACAGATGGATTCCTCTCTGCTGTGG 1197
 Qy 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 Db 1198 ACGGTTCCGTTGCTTCGCTTTGTACGTGAGATGATGAGTGTGAGGGGAGACAGAG 1257
 Qy 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 Db 1258 CCGTGTGTCGCTGCTTGGTTAATGATCGGTTGTCCTCGCTGCATGGGTGCTCCGGTGTAT 1317
 Qy 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 1318 GCTTTGGGAGATGATCCCGGATAGCTTTGTGAGGGGGTTGAGCTTTGTAGATCTGGG 1377
 Qy 442 GlyAspTrpAlaGluCysPheAla 449

Wed Oct 27 10:21:15 2004

Db	1378	GGTGATTGGCGGAGTGTTCCT 1401	Db	118	TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGCACCGTTCCTCTCTCTGGAAC 177
RESULT 5					
Sequence 33, Application US/09233510					
Patent No. 6350602					
GENERAL INFORMATION:					
APPLICANT: Robert F.M. Van Gorcom					
APPLICANT: Willem Van Hartingsveidt					
APPLICANT: Petrus A. Van Paridon					
APPLICANT: Anemarie E. Veenstra					
APPLICANT: Rudolf G.M. Luttin					
APPLICANT: Gerardus Selen					
TITLE OF INVENTION: Cloning and Expression of Microbial					
TITLE OF INVENTION: Phytase					
NUMBER OF SEQUENCES: 52					
CORRESPONDENCE ADDRESS:					
ADDRESSEE: Morrison & Foerster					
STREET: 545 Middlefield Road, Suite 200					
CITY: Menlo Park					
STATE: California					
COUNTRY: USA					
ZIP: 94025-3471					
COMPUTER READABLE FORM:					
MEDIUM TYPE: Floppy disk					
COMPUTER: IBM PC compatible					
OPERATING SYSTEM: PC-DOS/MS-DOS					
SOFTWARE: PatentIn Release #1.0, Version #1.25					
CURRENT APPLICATION DATA:					
APPLICATION NUMBER: US/09/233,510					
FILING DATE:					
CLASSIFICATION:					
PRIOR APPLICATION NUMBER: 07/688,578					
FILING DATE: 24-MAY-1991					
ATTORNEY/AGENT INFORMATION:					
NAME: Murashige, Kate H.					
REGISTRATION NUMBER: 29,959					
REFERENCE/DOCKET NUMBER: 24615-20026.00					
TELECOMMUNICATION INFORMATION:					
TELEPHONE: 415-327-7250					
TELEFAX: 415-327-2951					
INFORMATION FOR SEQ ID NO: 33:					
SEQUENCE CHARACTERISTICS:					
LENGTH: 1404 base pairs					
TYPE: nucleic acid					
STRANDEDNESS: double					
TOPOLOGY: linear					
MOLECULE TYPE: cdna to mRNA					
HYPOTHETICAL: NO					
ANTI-SENSE: NO					
ORIGINAL SOURCE:					
ORGANISM: Aspergillus ficuum (Aspergillus niger)					
STRAIN: NRRL 3135					
US-09-233-510-33					
Alignment Scores:					
Pred. No.: 1.31e-275					
Score: 2353.00					
Length: 1404					
Matches: 448					
Conservative: 0					
Percent Similarity: 100.00%					
Best Local Similarity: 100.00%					
Query Match: 99.79%					
Indels: 0					
Gaps: 0					
DB: 3					
US-10-089-364-4 (1-449) x US-09-233-510-33 (1-1404)					
QY	2	LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21	QY	362	ProLeuSerThrThrThrValGluAsnLleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db	58	CTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTCGATACGATCAGGGGTATCAA 117	Db	1138	CCGCTATCTACCAAGCCGCTGAGAAATATACCCAGACAGATGGATTCCTCTGCTTGG 119
QY	22	CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41	QY	382	ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401

Db 1198 ACGTTCCGTTGCTTCCGCTTTGACGTGCGAGATGATGACAGTGTGAGCGGAGCAGGAG 1257
 QY 402 ProLeuValArgValLeuValAsnAspArgValProLeuHisGlyCysProValAsp 421
 Db 1258 CGCTGGTCGCTGCTTGTGTTATGATCGCGTGTCCCGCTGCATGGGTCCGGTTGAT 1317
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 1318 GCTTTGGGAGATGATACCGCGGATAGCTTGTGAGGGGGTTGAGCTTTGCTAGATCTGG 1377
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 Db 1378 GGTGATTGGCGGAGTGTGTTGCT 1401

RESULT 6

US-08-151-574-31
 ; Sequence 31, Application US/08151574
 ; Patent No. 5436156
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert F.M. Van Gorcom
 ; APPLICANT: Willem Van Hartingsveldt
 ; APPLICANT: Petrus A. Van Paridon
 ; APPLICANT: Annemarie E. Veenstra
 ; APPLICANT: Rudolf G.M. Luttin
 ; APPLICANT: Gerardus Selten
 ; TITLE OF INVENTION: Cloning and Expression of Microbial
 ; TITLE OF INVENTION: Phytase
 ; NUMBER OF SEQUENCES: 52
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Morison & Foerster
 ; STREET: 545 Middlefield Road, Suite 200
 ; CITY: Menlo Park
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94025-3471
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; SOFTWARE:
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/151,574
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/688,578
 ; FILING DATE: 24-MAY-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murashige, Kate H.
 ; REGISTRATION NUMBER: 29,959
 ; REFERENCE/DOCKET NUMBER: 24615-20026.00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-327-7250
 ; INFORMATION FOR SEQ ID NO: 31:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6756 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Aspergillus ficuum (Aspergillus niger)
 ; STRAIN: NRRL 3135
 ; IMMEDIATE SOURCE:
 ; LIBRARY: lambda AF
 ; CLONE: pAF2-3, pAF2-6, pAF2-7
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 210..253
 ; FEATURE:

; NAME/KEY: intron
 ; LOCATION: 254..355
 ; FEATURE:
 ; NAME/KEY: exon
 ; LOCATION: 356..1715
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: join(210..253, 356..1715)
 ; OTHER INFORMATION: /codon_start= 210
 ; OTHER INFORMATION: /product= "Phytase"
 ; FEATURE:
 ; NAME/KEY: sig_peptide
 ; LOCATION: 210..380
 ; FEATURE:
 ; NAME/KEY: mat_peptide
 ; LOCATION: 381..1712
 ; IDENTIFICATION METHOD: experimental
 ; OTHER INFORMATION: /function= "inositol phosphate
 ; OTHER INFORMATION: phosphatase"
 ; OTHER INFORMATION: /product= "Phytase"
 ; OTHER INFORMATION: /evidence= EXPERIMENTAL
 ; US-08-151-574-31

Alignment Scores:

Pred. No.: 1.95e-274 Length: 6756
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservativeness: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 1 Gaps: 0

US-10-089-364-4 (1-449) x US-08-151-574-31 (1-6756)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 Db 369 CTGGCAGTCCCGCGCTCGAGAAATCAATCCAGTTGGCATACGGTCGATCAGGGGTATCAA 428
 QY 22 CysPheSerGluThrSerHisLeuTyrGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 Db 429 TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGTTCTTCTCTCTGCGCAAC 488
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 489 GAATCGGTATCTCCCTGAGTCCCGCGGATGAGATCACTTTTCGCTCAGGTCTCTC 548
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerHisGlyLysTyrSerAlaLeuIle 81
 Db 549 TCCCGTCATGGAGCGGTATCCGACGACTCCCAAGGGCAAGAAATATCGCTCTCAT 608
 QY 82 GluGluIleGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 609 GAGGATCCAGCAGAACGCGACCCACTTTGACGAAAAATATGCTTCTGAAACATAC 668
 QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
 Db 669 AACTACAGCTTGGGTGCAGATGACCTGACCTTCGAGAACAGGAGCTAGTCAATCC 728
 QY 122 GlyTleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 729 GGCATCAAGTCTACCAAGCGGTACGAATCGCTCACAAGGAACATCGTTCATTCATCCGA 788
 QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysPheIleGluGlyPheGlnSer 161
 Db 789 TCCTCTGGCTCCAGCGCGGTATCGCTCCGCGAAGAAATTCATCGAGGGCTTCAGAGC 848
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAsnVal 181
 Db 849 ACCAAGCTGAGGATCTCTGTCGCCAGCCCGCCCAATCGTCCGCCAAGATCGAGCTGCTC 908
 QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 Db 909 ATTTCCGAGGCCAGCTCATCCCAACAACACTCTCGACCCAGGCACCTGCTCTTCCGAA 968

QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerile 221
DB 969 GACAGCGAATGGCGGATACCGTGAAGCAATTTCCAGCCACGTTGTCCTCCCTCCAT 1028
QY 222 ArgGlnArgLeuGluAlaAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
DB 1029 CGTCAACGTCGTGAGACGACACCTGTCGCGTGACTCTCACAGACACAGAGTGACCTAC 1088
QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrValAspThrLysLeuSer 261
DB 1089 CTCATGGACATGTCTCTTCGACACCATCTCCACCAGACCGCTCCACACCAAGCTGTC 1148
QY 262 ProPheCysAspLeuPheThrHisAspGluTyrIleAsnTyrAspTyrLeuGlnSerLeu 281
DB 1149 CCTCTCTGACCTGTTCACCCAGCAAGATGATCACTACGACCTCTCCAGCTCTCTG 1208
QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
DB 1209 AAAAGATATACGCCCATGTGTGAGGTAAACCGCTCGGCCGACCCAGGCGTGGCTAC 1268
QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerAsn 321
DB 1269 GCTAACGAGCTCATCGCCGCTCTGACCCACTCGCTGTCCACGATGACACCACTTCAAC 1328
QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
DB 1329 CACACTTTGACCTGAGCCCGGCTACCTTTCCGCTCACTCTACTCTCTACGGGACTTT 1388
QY 342 SerHisAspAsnGlyIleIleSerileLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
DB 1389 TCAGTACGACACCGCATCACTCCATCTCTTTGCTTTAGTCTGTACACCGCACTAAG 1448
QY 362 ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
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RESULT 7

US-08-419-448-31

Sequence 31, Application US/08419448

Patent No. 5863533

GENERAL INFORMATION:

APPLICANT: Robert F.M. Van Gorcum

APPLICANT: Willem Van Hartingsveldt

APPLICANT: Petrus A. Van Paridon

APPLICANT: Annemarie B. Veenstra

APPLICANT: Rudolf G.M. Luttin

APPLICANT: Gerardus Seltin

TITLE OF INVENTION: Cloning and Expression of Microbial

TITLE OF INVENTION: Phytase

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Ave. N.W., Suite 5500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,448
FILING DATE: 10-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 6756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Aspergillus ficuum (Aspergillus niger)
STRAIN: NRRL 3135
IMMEDIATE SOURCE:
LIBRARY: lambda AF
CLONE: pAF2-3, pAF2-6, pAF2-7
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RESULT 8
US-09-233-510-31
; Sequence 31, Application US/09233510
; Patent No. 6350602
; GENERAL INFORMATION:
; APPLICANT: Robert P.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,510
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus ficuum (Aspergillus niger)
; STRAIN: NRRL 3135
; IMMEDIATE SOURCE:
; LIBRARY: lambda AF
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; LOCATION: 210..253

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; Sequence 7, Application US/07923724
; Patent No. 5780292
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosk, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerstr m, Richard B.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; TITLE OF INVENTION: in Trichoderma
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
```

CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/923,724
 FILING DATE: 31-JUL-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/496,155
 FILING DATE: 19-MAR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/044,077
 FILING DATE: 29-APR-1987
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: UK 8610600
 FILING DATE: 30-APR-1986
 ATTORNEY/AGENT INFORMATION:
 NAME: Gimbala, Michele A.
 REGISTRATION NUMBER: 33,851
 REFERENCE/DOCKET NUMBER: 1050.0240004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2363 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: both
 FEATURE:
 NAME/KEY: CDS
 LOCATION: join(404...447, 550...1906)
 US-07-923-724-7

Alignment Scores:
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GENERAL INFORMATION:
APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Ramosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerstr m, Richard B.
APPLICANT: Houston, Christine S.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESS: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM: disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,426A
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Grant E.
REGISTRATION NUMBER: P-41,264
REFERENCE/DOCKET NUMBER: 1050.0080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2363 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: join(404..447, 550..1906)
US-08-609-426A-7

Alignment Scores:
Pred. No.: 7,15e-270 Length: 2363
Score: 2309.00 Matches: 436
Percent Similarity: 99.11% Conservativeness: 8
Best Local Similarity: 97.32% Mismatches: 4
Query Match: 97.92% Indels: 0
DB: 2 Gaps: 0

US-10-089-364-4 (1-449) x US-08-609-426A-7 (1-2363)

Qy 2 LeuAlaValProAlaSerArgAsnGlnSerCysAspThrValAspGlnGlyTyrGln 21

Db 563 CTGGCAGTCCCGCGCTCGAGAAATCAATCCACTTGGCATCGGTCAAGGGTATCAA 622

Qy 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
Db 623 TGCCTTCTCGAGACTTCGCATCTTTGGGGTCAATAGCGCGCGTCTTCTCTCTGCGCAAC 682
Qy 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db 683 GAATCGGCCATCTCCCTGATGTGCGCGCGGGTTGCAGAGTCACTTTCGCTCAGGTCTC 742
Qy 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeu 81
Db 743 TCCGTCATGAGCGCGGTATCGACCGAGTCCAGGGCAAGAAATACCTCCGCTCTCAT 802
Qy 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db 803 GAGGAGATCCAGCAAGACCTGACCCACTTTGATGGAATAATATGCTTCTGAAGACATAC 862
Qy 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGlnGlnLeuValAsnSer 121
Db 863 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGAGAGCAGAGCTAGTCAACTCC 922
Qy 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db 923 GGCATCAAGTCTTACCAGCGATACGAATCGCTCACAAGGAACATCAATTCGTTTCATCGA 982
Qy 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
Db 983 TCCCTCTGGCTCCAGCGCGGTGCTCGCGGAGAAATTCATTGAGGGCTTCCAGAGC 1042
Qy 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db 1043 ACCAAGCTGAAGGATCTCGTGCAGCGGGCCAATCGTCGCCCAAGATCGACGTGGTC 1102
Qy 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
Db 1103 ATTTCGAGCGCCAGCTCATCAACAACTCTCGACCCAGGACCTGCACTGCTTTTGA 1162
Qy 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db 1163 GACAGCGAATTCGCCGATACCGTCAAGCAATTCACCGCCACGTTGCGCCCTCCATT 1222
Qy 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db 1223 CGTCAAGCTCTGGAGAACGACCTGTCTGGCGTGACTCTCACACACAGAAAGTGACCTAC 1282
Qy 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db 1283 CTCATGGACATGTGCTCTTCGACACCATCTCCACACGACCCGTCGACACCAAGCTGTCC 1342
Qy 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
Db 1343 CCCTTCTGTGACCTGTTCACCATGACGAATGGATCCACTACGACTACCTCCAGTCCCTG 1402
Qy 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db 1403 AAAAAATACTACGCGCATGCGCAGGTAAACCCGCTCGCCCGCCACCGCGCGCTCGGCTAC 1462
Qy 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
Db 1463 GCTAACGAGCTCATGCCCGCTCTCACCCACTCGCCTGTCCCGTGTCCAGTGTACACAGCTCAAC 1522
Qy 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db 1523 CACACCTTGGACTCGAACCAGCTACCTTCGCGTCAACTCTACTCTCTACGCGGAGCTTT 1582
Qy 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db 1583 TCCACGATAACGGCATCATCTCTATCTCTTTGCTTTGGGTCTGTACACAGGCACTAAG 1642
Qy 362 ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db 1643 CCGCTGTCTACACGACCGGTGGAGATATCACCCAGACAGATGGGTCTCGTCTGCTTGG 1702

QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspThrSerSerAsn 321
Db 1479 GCTAACGAGCTCATGCCCGCTCCACCACTCGCTGTCCAGTACACACAGCTCCAAAC 1538
QY 322 HisThrLeuAspSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db 1539 CACACCTTGAGCTCGAACCCAGCTACTCCCGCTCAACTCTACTCTCTACGGGACTTT 1598
QY 342 SerHisAspAsnGlyIleLeuSerLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db 1599 TCCACGATAACGGCATCATCTCTATCTCTTGTCTTGGTCTGTACACACGGCACTAAG 1658
QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
Db 1659 CCGCTGTCTACCAACGCGTGGAGATATACCCACAGACAGATGGGTCTCTGCTGTGG 1718
QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
Db 1719 ACGGTTCGGTTCCTTCGGCTCTGTACGTGAGATGATGTCAGTCCAGGCCGAGCAGGAG 1778
QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db 1779 CCGCTGTCTGTCTGTGTAAATGATCGGTGTTCCTCCGCTGCATGGGTGTCCAAATGAT 1838
QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db 1839 GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGGTTGAGCTTTGTCTAGATCUGG 1898
QY 442 GlyAspTyrAlaGluCysPheAla 449
Db 1899 GGTGATGGCGAGTGTTCTGCT 1922

RESULT 12

US-09-155-855-5

; Sequence 5, Application US/09155855

; Patent No. 613902

; GENERAL INFORMATION:

; APPLICANT: KONDO, Hidemasa

; APPLICANT: ANAZAWA, Hideharu

; APPLICANT: KANEKO, Syunichi

; APPLICANT: NAGASHIMA, Tadashi

; APPLICANT: TANGE, Tatsuya

; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE

; FILE REFERENCE: 81356/124

; CURRENT APPLICATION NUMBER: US/09/155,855

; CURRENT FILING DATE: 1998-10-05

; EARLIER FILING DATE: 1997-04-04

; EARLIER APPLICATION NUMBER: WO PCT/JP97/01175

; EARLIER APPLICATION NUMBER: JP 084314

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 1515

; ORGANISM: Aspergillus niger

; FEATURE:

; NAME/KEY: sig_peptide

; LOCATION: (1)..(45)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)..(45)

; FEATURE:

; NAME/KEY: sig_peptide

; LOCATION: (157)..(183)

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: (184)..(1512)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (157)..(1512)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (157)..(1512)

; US-09-155-855-5

Alignment Scores:

Pred. No.: 1,95e-266 Length: 1515
Score: 2278.00 Matches: 427
Percent Similarity: 98.44% Conservative: 14
Best Local Similarity: 95.31% Mismatches: 7
Query Match: 96.61% Indels: 0
DB: 3 Gaps: 0

US-10-089-364-4 (1-449) x US-09-155-855-5 (1-1515)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
Db 169 CTGGCAGTCCCGCTCGAGAAATCAATCCACTTCGGATACCGTCCATCAGGGGTATCAA 228
QY 22 CysPheSerGluThrSerHisLeuTyrGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
Db 229 TGTCTTCGGAGACTTCGCATCTTTGGGGCCATATACGCCCGTCTCTTCTCTGGCAAC 288
QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db 289 AAATCGCCATCTCCCTCATGTTCTCGCGATGCCATGTCACTTCGCCACGATCTC 348
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
Db 349 TCCCGCATGGAGACGGTATCCGACCGACTCCAGGGCAAGAAATACTCCGCTCTCATC 408
QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db 409 GAGGAGATCCAGCAGAACCGGACAACTTCGAGGGGAATATGCTTCCTGAACATAC 468
QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db 469 AACTACAGCCTGGCGCGGATGATCTGACTCCCTTCGGAGCAGGAGCTGGTCAACTCC 528
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db 529 GGGCTCAAGTCTTACCAGCGATACGAATCGCTCACAAGAAACATGTGCCGCTCATCCGA 589
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
Db 589 TCTCTAGGCTCCAGCGCGGATGCTCTGGCAATTAATTCATCGAGGGCTTCCAGAGC 648
QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db 649 ACTAAGCTGAAGGATCTCTGTCGCCAGCCGCAATCGTCGCCCAAGATCGAGTGTCTC 708
QY 182 IleSerGluAlaSerSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
Db 709 ATTTACAGAGCCAGCATCCACACACTCTCGATCCGGGACCTCGACCGTTTTCGAA 768
QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db 769 GATAGCGAATTTGGCCGATGACATCGAAGCCAAATTCACCGCAGGTTCTGTCCTCCATT 828
QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db 829 CGTCAACGTCCTGGAGAACGACTTGTCTGGCGTGTCTCTCAGCGACACAGAGTGCCTAC 888
QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db 889 CTCATGGACATGTCTCTTCGACACCATCTCCACCGAGCCCGTCGACACCAAGCTGTCC 948
QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
Db 949 CCTTCTGTGACCTGTTCCCATGAAGATGGATCAACTAGACTACTACCTCCAGTCCCTG 1008
QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db 1009 AACAAATACTACGGCCATGGCGCAGTAACCGCTCGGCCGACCCAGGGGCTGGGTAC 1068
QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321

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Db 1069 GCTAACGAGCTCATGCCCGCTCTCAACCACTCGCTGTCCACGATGACACACGCTCCCAAC 1128
Qy 322 HistThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db 1129 CACACATTTGGATCTCAACCCGGCTACTTTCCCGCTCACTCACTCTCTATCGGACTTT 1188
Qy 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db 1189 TCGCATGATAACGGCATCATCTCTATCTCTCTTTTGGTCTGTACAAACGGACCAAG 1248
Qy 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
Db 1249 CGCGTGTCTTTCACACCGCGGAGATATCACCCAGACGATGGTCTCTCACTCGCTGG 1308
Qy 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysAlaGluGlnGlu 401
Db 1309 ACGGTCTCTTTCGCGTCCGCGATGTACGTGAGATGATGCAATGACGATCCGAGCAGGAG 1368
Qy 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db 1369 CCTTTGGTCCGTGTCTGTGTTAATGATCGTGTGTTCGCTGCATGGCTGTCCGTTGAT 1428
Qy 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db 1429 GCTTTGGGAAGATGTACCGCGGATAGCTTCGTGAAGGGGTTGAGCTTTGCCAGATCTGGC 1488
Qy 442 GlyAspTrpAlaGluCysPheAla 449
Db 1489 GGTGATTTGGGGGAGTGTTCGCT 1512

RESULT 13
US-09-543-744-5
; Sequence 5, Application US/09543744
; Patent No. 6309870
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/543,744
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(45)
; NAME/KEY: CDS
; LOCATION: (1)..(45)
; NAME/KEY: sig_peptide
; LOCATION: (157)..(183)
; NAME/KEY: mat_peptide
; LOCATION: (184)..(1512)
; NAME/KEY: CDS
; LOCATION: (157)..(1512)
US-09-543-744-5

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Alignment Scores:
Pred. No.: 1.95e-266 Length: 1515
Score: 2278.00 Matches: 427
Percent Similarity: 98.44% Conservative: 14
Best Local Similarity: 95.31% Mismatches: 7
Query Match: 96.61% Indels: 0

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DB: 3 Gaps: 0
US-10-089-364-4 (1-449) x US-09-543-744-5 (1-1515)
Qy 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
Db 169 CTGGCAGTCCCGCGCTCGAGAAATCAATCCACTTCGATACGTCGATCAGGGGTATCAA 228
Qy 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaSer 41
Db 229 TGTCTTCTCGGAGACTTCGATCTTTGGGGCCAATAACGGCGCGTCTTTTCTCTGCAAAAC 288
Qy 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db 289 AAATCGGCATCTCCCTGATGTTCTCCGATGCCATGTCACTTTCGCCCGGTCTTC 348
Qy 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
Db 349 TCCCGCCATGGAGCACCGGTATCCGACCGACTCCAAGGGCAAGAAATATCTCCGCTCTCATC 408
Qy 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db 409 GAGGAGATCCAGCAGAACCGCACACCTTCGAGGGGAAATATGCTCTCTCGAAGACATAC 468
Qy 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db 469 AACTACAGCTTGGGCGCGGATGATCTGACTCCCTTCGGAGAGAGGAGCTGGTCAACTCC 528
Qy 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db 529 GCGGTCAAGTTCTACCGAGCATACGAATCGCTCACAGAAACATGTCCCGTTCATCCGA 588
Qy 142 SerSerGlySerSerArgValIleAlaSerGlyLysPheIleGluGlyPheGlnSer 161
Db 589 TCCTCAGGCTCCAGCGCGTGAATTCCTCTCGCAATAAATTCATCGAGGGGTTCAGAGC 648
Qy 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db 649 ACTAAGCTGAAGGATCTCTGTCGCCCGCGCCCAATCGTCCGCCAAGATCGAGTGTGTC 708
Qy 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
Db 709 ATTTTCAGAGGCCAGCATCCCAACACACTCTCGATCCGGSCACCTGCACCGTTTCGAA 768
Qy 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db 769 GATAGCGAATTGGCCGATGATCAAGAGCAATTCACCGCCAGCTTCGTCCTCCCTCCATT 828
Qy 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db 829 CGTCAACGTCTGGAGAGGACTTGTCTGGCGTGTCTCTCAGGACACAGAAAGTGCCTTAC 888
Qy 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db 889 CTCATGGACATGTCTCTTCGACCATCTCCACCGAGCCGTCGACACCAAGCTGTCC 948
Qy 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
Db 949 CCCTTCTGTGACCTGTTCACCCATGAAGAATGATCAACTACGACTACCTCCAGTCCCTG 1008
Qy 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db 1009 AACAAATCTACGGCCATGGCGGAGTAACCGCTCCGGCCGACCCAGGGGCTCGGTAC 1068
Qy 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
Db 1069 GCTAACGAGCTCATCGCCCGCTCTCACCATCTCGCTCTCCAGATGACACAGCTCCAAAC 1128
Qy 322 HistThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db 1129 CACACATTTGGACTCAACCCGGGTACTTTCCCGCTCACTCACTCTCTATGCGGACTTT 1188
Qy 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361

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Db      1189 TCGCATGATACGGGATCATCTATCTCTTTGGTCTGTACACGGCACCAG 1248
QY      362 ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db      1249 CCGCTGTCTTCCAGCAGCGGAGAAATATCAACCAGACCGATGGGTCTCATCTGCCTGG 1308
QY      382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
Db      1309 ACGGTTCCTTTCCGCTCGGCGATGTACGTGAGATGATCAATGCCAGTCCGAGCAGGAG 1368
QY      402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db      1369 CTTTGGTCCGTGCTGTGTTAATGATCGTGTTCCTCCGCTCATGCGTGTCCGGTGTAT 1428
QY      422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db      1429 GCTTTGGGAAGATGTACGGGGATAGCTTCGTGAGGGGTGAGCTTTGCCAGATCTGGC 1488
QY      442 GlyAspTrpAlaGluCysPheAla 449
Db      1489 GGTGATTGGGGGAGTGTTCGGCT 1512

RESULT 14
US-09-929-060-5
; Sequence 5, Application US/09929060
; Patent No. 6548282
; GENERAL INFORMATION:
; APPLICANT: KONDO, HIDEMASA
; APPLICANT: ANAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI
; APPLICANT: TANGE, TAIJOYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/929,060
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314/1996
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 5
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(45)
; NAME/KEY: CDS
; LOCATION: (157)..(1512)
US-09-929-060-5

Alignment Scores:
Pred. No.: 1.95e-266 Length: 1515
Score: 2278.00 Matches: 427
Percent Similarity: 98.44% Conservative: 14
Best Local Similarity: 95.31% Mismatches: 7
Query Match: 96.61% Indels: 0
DB: 4 Gaps: 0

US-10-089-364-4 (1-449) x US-09-929-060-5 (1-1515)
QY      2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
Db      169 GTGGAGTCCCGCTCGAGAAATCAATCCACTTGGATAGCGTTCGATCAGGGGTATCAA 228
QY      22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
Db      229 TGCCTTCGAGACTTCGCACTCTTTGGGGCCAAATACGCGCGCTTCTTTCTCTGCGCAAAC 288

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QY      42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db      289 AAATGGCCCATCTCCCTCATGTCTCTGCGGATGCCATGTACATTCCTGCCAGGTTCTC 348
QY      62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaIle 81
Db      349 TCCCGCCATGGAGCAGGTATCCGACCGACTCAAGGGCAAGAAATATCTCCGCTCTCATC 408
QY      82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db      409 GAGGAGATCCACAGAACCGCACCTTCGAGGGGAATATATGCCCTTCTGAGACATATC 468
QY      102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSer 121
Db      469 AACTACAGCTGGCGCGGATGATCTGACTCCCTTCGGAGAGCAGGAGTGGTCAACTCC 528
QY      122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db      529 GCGCTCAAGTTCTACCCAGCGATACGAATCGCTCACAGAAACATTCCTCCGTTTCATCCGA 588
QY      142 SerSerGlySerSerArgValIleAlaSerGlyLysPheIleGluGlyPheGlnSer 161
Db      589 TCTCAGGCTCCAGCCGCTGATTGCTCTGGCAATAAATCATCGAGGGCTTCAGAGC 648
QY      162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db      649 ACTAAGCTGAGGATCTCTGTCGCCAGCCGGCCAAATCGTCCGCCAAGATCGACGTGGTC 708
QY      182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
Db      709 ATTTCAGAGCGACGACATCCAAACACTCTCGATCCGGGCACTCGCACCGCTTTTCGAA 768
QY      202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db      769 GATAGCGAATTGGCCGATGACATCGAAGCCAAATTCACGCCACGTTGTCCTCCCTCAAT 828
QY      222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db      829 CGTCAACGCTGGAGAACGACTTGTCTGGCGTCTCTCACGGACACAGAAAGTACCTAC 888
QY      242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db      889 CTCATGGACATGTGCTCTTCGACACCATCTCCACCAGCACCCGTCGACACCAAGCTCTCC 948
QY      262 ProPheCysAspLeuPheThrHisAspGluTyrIleAsnTyrAspTyrLeuGlnSerLeu 281
Db      949 CCCTTCTGTGACCTGTTTACCCATGAAGATGATGATGATGATGATGATGATGATGATG 1008
QY      282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db      1009 AACAAATACTACGGCCATGGCGCAGGTAAACCCGCTCGGCCGCCACCCAGGCGTCCGCTAC 1068
QY      302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
Db      1069 GCTAACGAGCTCATCGCCCGCTCTCACCCACTCGCCCTGTCCAGATGATGATGATGATGATG 1128
QY      322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db      1129 CACATTTGGACTTCCAAACCGGGTACTTTCGGCTCAACTCCACTCTCTATGCGGACTTT 1188
QY      342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db      1189 TCGCATGATAAGGCAATCATCTCTATCTCTTTGCTTGGGTCTGTATCAACAGGCGCACCAAG 1248
QY      362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db      1249 CCGTGTCTTCCACGACCGCGGAGAAATATACCCAGACCCGATGGGTCTCATCTGCTCTGG 1308
QY      382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
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QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db 1369 CTTTGGTCCGTCCTTGGTTAATGATCGTGTGTCCTCGCTGCAUGGCTGTCCGGTTGAT 1428
QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
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RESULT 15
US-09-155-855-4
; Sequence 4, Application US/09155855
; Patent No. 6139902
; GENERAL INFORMATION:
; APPLICANT: KONDO, Hidemasa
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: KANEKO, Syunichi
; APPLICANT: NAGASHIMA, Tadashi
; APPLICANT: TANGE, Tatsuya
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 81356/124
; CURRENT APPLICATION NUMBER: US/09/155,855
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: WO PCT/JP97/011175
; EARLIER FILING DATE: 1997-04-04
; EARLIER APPLICATION NUMBER: JP 084314
; EARLIER FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1332
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1332)
US-09-155-855-4

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Percent Similarity: 98.42% Conservative: 14
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Query Match: 95.63% Indels: 0
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US-10-089-364-4 (1-449) x US-09-155-855-4 (1-1332)

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QY 27 SerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGluSerValIleSer 46
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QY 47 ProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyAla 66
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QY 67 ArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGluGluIleGln 86
Db 181 CGGTATCCGACCGACTCCAGGGCAAGAAATACCTCCGCTCTCATCGAGAGATCCAGCAG 240
QY 87 AsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsnTyrSerLeuGly 106
Db 241 AACCGCAACACTTCGAGGGGAATATGCTTCCTGAGACATACACTACAGCTGGGC 300
QY 107 AlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGlyIleLysPheTyr 126

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Search completed: October 24, 2004, 17:26:17
Job time : 175 secs

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Db 361 CAGCGATACGAATCGCTCACAAGAAACATTTGTCGCTTCATCCGATCTCTCAGGCTCCAGC 420
QY 147 ArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLysLeuLysAsp 166
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QY 167 ProArgAlaGlnProGlyGlnSerSerProLysIleAspValIleSerGluAlaSer 186
Db 481 CCTCGTCCAGCCCGGCCAATCGTCGCCCAAGATCGACGTGGTCAATTCAGAGGCCAGC 540
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QY 287 HisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAlaAsnGluLeuIle 306
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QY 307 AlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHisThrLeuAspSer 326
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QY 327 SerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGly 346
Db 961 AACCGCGCTACTTTCGCGCTCACTCCACTCTCATGCGGACTTTTCGATGATAACGCGC 1020
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Db 1021 ATCATCTCTATCTCTTGTGTTGCTGTACAAACGACCAAGCGCTGTCTTCCAGC 1080
QY 367 ThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaThrThrValProPheAla 386
Db 1081 ACCCGGAGAAATATCACCCAGACCGATGGGTCTCTCATCTGCTCGACGGTTCCTTTCGCG 1140
QY 387 SerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluProLeuValArgVal 406
Db 1141 TCGCGCATGTCAGTCGAGATGATGCAATGCGATGCCAGGAGGAGCCCTTTGGTCCGTC 1200
QY 407 LeuValAsnAspArgValValProLeuHisGlyCysProValAspAlaLeuGlyArgCys 426
Db 1201 TTGTTAATGATCGTGTGTTTCGCTGTCATGGCTGTCCGGTTGATGCTTTTGGGAGATGT 1260
QY 427 ThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGlu 446
Db 1261 ACGGCGATAGCTTCGTAAGGGGTTGAGCTTTGCCAGATCTCGCGGTGATTGGGGGAG 1320
QY 447 CysPheAla 449
Db 1321 TGTTTCGCT 1329

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 12:59:09 ; Search time 828 Seconds
(without alignments)
2846.606 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

Sequence: 1 MLAVPASRNQSSCDTVDQGY.....SFVGLSFARSGDWAECFA 449

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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8: geneseqn2003as:*
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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2358	100.0	1350	4	AAD03283 Aspergill
2	2358	100.0	1449	4	AAD03287 Carrot ex
3	2353	99.8	1344	6	ABN85591 Aspergill
4	2353	99.8	1382	6	ABN85587 Aspergill
5	2353	99.8	1289	6	ABN85590 Aspergill
6	2353	99.8	1404	2	AAQ11175 Chromosom

7	2353	99.8	1404	2	AAZ27421	A. ficcum
8	2353	99.8	1506	6	ABN85588	Aspergill
9	2353	99.8	2665	12	ADL91241	Wild-type
10	2353	99.8	6756	2	AAQ11174	Sequence,
11	2353	99.8	6756	2	AAT65137	Aspergill
12	2353	99.8	6756	8	ABX13436	Plasmids
13	2350	99.7	1344	6	ABN85592	Aspergill
14	2350	99.7	2665	12	ADL91267	Mutant ph
15	2350	99.7	2665	12	ADL91261	Mutant ph
16	2349	99.6	2665	12	ADL91263	Mutant ph
17	2349	99.6	2665	12	ADL91247	Mutant ph
18	2349	99.6	2665	12	ADL91259	Mutant ph
19	2349	99.6	2665	12	ADL91257	Mutant ph
20	2349	99.6	2665	12	ADL91273	Mutant ph
21	2348	99.6	1404	2	AAT65136	Aspergill
22	2347	99.5	2665	12	ADL91255	Mutant ph
23	2347	99.5	2665	12	ADL91271	Mutant ph
24	2347	99.5	2665	12	ADL91269	Mutant ph
25	2347	99.5	2665	12	ADL91245	Mutant ph
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33	2342	99.3	2665	12	ADL91283	Mutant ph
34	2341	99.3	1404	2	AAQ13878	Phytase g
35	2341	99.3	2665	12	ADL91291	Mutant ph
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40	2327	98.7	2665	12	ADL91295	Mutant ph
41	2309	97.9	2363	2	AAQ58126	Phytase g
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ALIGNMENTS

RESULT 1

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ID AAD03283 standard; DNA; 1350 BP.

XX AC AAD03283;

DT 13-JUN-2001 (first entry)

DE Aspergillus niger phytase (Phy) A-1 gene.

XX KW Phytase A; Phy; plant productivity; phosphorus utility;
KW biomass production; hypocotyl production; epicotyl production;
KW transgenic plant; phytate; ds.
XX OS Aspergillus niger.

XX Key Location/Qualifiers

FT CDS 1..1350

FT /*tag= a

FT /product= "Aspergillus niger phytase A-1 protein"

XX WO200122806-A1.

XX PD 05-APR-2001.

XX PF 22-SEP-2000; 2000WO-AU001183.

XX PR 24-SEP-1999; 99AU-00003049.

XX PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

PA (AUWO-) AUSTRALIAN WOOL RES & PROMOTION ORG.
 XX Richardson AE, Hayes JE, Simpson RJ;
 PI P-PSDB; AAY72974.
 DR WPI; 2001-244964/25.
 XX
 XX
 XX
 PT New isolated nucleic acid encoding a mature phytase polypeptide for
 PT enhancing the phosphorus nutrition of a plant, the growth of a plant on a
 PT phosphorus source and the phosphorus content of a plant.
 XX
 XX
 PS Claim 7; Page 121-124; 144pp; English.
 XX
 CC The invention relates to a method of modifying plant productivity which
 CC involves expressing phytase (Phy) A gene from *Aspergillus niger*, in a
 CC plant cell. Phytase gene is capable of facilitating plants ability to
 CC utilise soil phosphorus. It is used to enhance the phosphorus nutrition
 CC of a plant or the growth of a plant on a phosphorus source comprising
 CC phytate and/or increase the phosphorus content of a plant. This gene is
 CC used to enhance the biomass produced by a plant and also to enhance the
 CC rate of hypocotyl production or the rate of epicotyl production.
 CC transgenic plant containing phytase gene has improved productivity than
 CC its isogenic counterparts. The present sequence is *Aspergillus niger* Phy
 CC A-1 gene. This gene is modified (Phy A-2 gene) in order to bring about
 CC suitable expression in plant cells
 XX
 SQ Sequence 1350 BP; 288 A; 419 C; 332 G; 311 T; 0 U; 0 Other;

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 Score: 2358.00 Matches: 449
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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US-10-089-364-4 (1-449) x AAD03283 (1-1350)

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 DB 61 CAAATGCTCTCCGAGACTTGGCATCTTTGGGGTCAATACGACCGCTTCTCTCTGGCA 120
 QY 41 AsnGluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnVal 60
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 QY 61 LeuSerArgHisGlyAlaArgTyrProThrAspSerIlysglyLysTyrSerAlaLeu 80
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 DB 241 ATTGAGGAGTCCAGCAGAAGCGACCACTTTGACGGAAATATGCTTCTCGAAGACA 300
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 QY 121 SerGlyLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIle 140
 DB 361 TCCGGCATCAAGTTCTACAGCGGTACGAATCGCTCACAGGAACATCGTTCCATTATC 420
 QY 141 ArgSerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGln 160
 DB 421 CGATCCCTCTGGTCCAGCCGCGTATCGCTCCGGCAAGAAATTCATCGAGGGCTTCCAG 480
 QY 161 SerThrIlyLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspVal 180
 DB 481 AGCACCAGGTGAAGGATCTCTCGTCCCGAGCCCGGCCAATCGTCGCCCAAGATCGACGTG 540

QY 181 ValIleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPhe 200
 DB 541 GTCATTTCCGAGGCCAGCTCATCCAAACACTCTCGAGCCAGGACCTGCACTGTCTTC 600
 QY 201 GluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSer 220
 DB 601 GAAGACAGGAATTTGGCCGATACCGTCGAAGCAATTTACCGCCACGTCGTCCTCCCTCC 660
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 QY 361 LysProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAla 380
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 DB 1141 TGGACGGTTCCGTTTCTGCGGTTTGTACGTGAGATGATGATGATGATGATGATGATGAT 1200
 QY 401 GluProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProVal 420
 DB 1201 GAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
 QY 421 AspAlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSer 440
 DB 1261 GATGCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGGTGTGAGCTTTGTAGATCT 1320
 QY 441 GlyGlyAspTrpAlaGlnCysPheAla 449
 DB 1321 GGGGGTCAITGGCGGAGTGTGTTTGTCT 1347

RESULT 2
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 ID AAD03287 standard; DNA; 1449 BP.
 XX
 AC AAD03287;
 XX
 XX 11-SRP-2003 (revised)
 DT 13-JUN-2001 (first entry)
 XX
 DE Carrot extensin leader peptide-A. niger phytase A-1 chimeric gene.
 XX
 KW Phytase A; Phy; plant productivity; phosphorus utility;
 KW biomass production; hypocotyl production; epicotyl production;
 KW transgenic plant; phytate; carrot; extensin; ds.
 XX
 OS *Daucus carota*.

OS Aspergillus niger.
 XX Chimeric.

Key Location/Qualifiers
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 /tag= c
 /product= "Mature carrot extensin leader peptide- A.
 niger phytase A-1 chimeric protein"
 WO200122806-A1.
 XX 05-APR-2001.
 XX 22-SEP-2000; 2000WO-AU001183.
 XX 24-SEP-1999; 99AU-00003049.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (AUWO-) AUSTRALIAN WOOL RES & PROMOTION ORG.
 XX Richardson AE, Hayes JE, Simpson RJ;
 PI WPI: 2001-244964/25.
 DR P-PSDB; AAY72978.
 XX New isolated nucleic acid encoding a mature phytase polypeptide for
 PT enhancing the phosphorus nutrition of a plant, the growth of a plant on a
 PT phosphorus source and the phosphorus content of a plant.
 XX Claim 9; Fig 1; 144pp; English.

The invention relates to a method of modifying plant productivity which
 CC involves expressing phytase (Phy) A gene from Aspergillus niger, in a
 CC plant cell. Phytase gene is capable of facilitating plants ability to
 CC utilise soil phosphorus. It is used to enhance the phosphorus nutrition
 CC of a plant or the growth of a plant on a phosphorus source comprising
 CC phytate and/or increase the phosphorus content of a plant. This gene is
 CC used to enhance the biomass produced by a plant and also to enhance the
 CC rate of hypocotyl production or the rate of epicotyl production.
 CC Transgenic plant containing phytase gene has improved productivity than
 CC its isogenic counterparts. The present sequence is carrot extensin leader
 CC peptide-A. niger phytase A-1 chimeric gene. This chimeric gene is used to
 CC enhance phosphorus nutrition in plants. (Updated on 11-SEP-2003 to
 CC standardise OS field)

XX Sequence 1449 BP; 312 A; 439 C; 355 G; 343 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 6,14e-235 Length: 1449
 Score: 2358.00 Matches: 449
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-089-364-4 (1-449) x AAD03287 (1-1449)

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 DB 160 CAATGCTTCTCGAGACTTCGACTTTGGGGTCAATACGACACCGCTTCTTCTCTGGCA 219

QY 41 AsnGluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnVal 60

DB 220 AACGAATCGGTCACTCCCTGAGTGGCGCGGATGAGAGTCACTTCGCTCAGGTC 279

QY 61 LeuSerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeu 80

DB 280 CTTCTCCCGTCATGGAGCGCGGTATCCGACCGACTCCAGAGGCAAGAAATACTCCGCTCTC 339

QY 81 IleGluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThr 100

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DB 580 AGCACCAAGCTGAGGATCTCTGTCGCCAGCCCGGCAATCGTCCCAAGATCGACGTG 639

QY 181 ValIleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPhe 200

DB 640 GTCATTTCCGAGGCCAGCTCATCCAAACAACACTCTCGACCCAGGACCTGCACTGTCTTC 699

QY 201 GluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSer 220

DB 700 GAAGACACGGAAATGGCCGATACCGTCGAAGCAATTTACCGCCACGTTCTGTCCTCTCC 759

QY 221 IleArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThr 240

DB 760 ATTCTCAACGCTCGAGAACGACCTGTCGGTGTGACTCTCACAGACACAGAGTGAAC 819

QY 241 TyrLeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeu 260

DB 820 TACTCTCATGGACATGTGCTCTTCGACACCATCTCCACAGCACCGCTCGACACCAAGTG 879

QY 261 SerProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSer 280

DB 880 TCCCCCTTCTGTGACCTGTTACCCCAAGCAATGATCACTACGATACCTCTCCAGTCC 939

QY 281 LeuLysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGly 300

DB 940 TTGMAAAGATTATTACGGCCATGGTGCAGGTAAACCGCTCGGCCGACCCAGGCGCTCGGC 999

QY 301 TyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSer 320

DB 1000 TACGCTAACGAGCTCATCGCCCGTCTGACCCACTCGCTGTCCAGATGACACCACTTCC 1059

QY 321 AsnHisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAsp 340

DB 1060 AACACACTTTGGACTCGAGCCCGGCTACCTTTTCGCTCAACTCTACTCTCTTACCGGAC 1119

QY 341 PheSerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThr 360

DB 1120 TTTTCGATGACAACGGCATCATCTCCATTCTTTTGGTCTGTGTACACGGCACT 1179

QY 361 LysProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAla 380

DB 1180 AAGCGGTATCTACACGACCGTGGAGAAATATACCCAGACAGATGGATTCTCGTCTGCT 1239

QY 381 TrpThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGln 400

DB 1240 TGGACGGTTCCGTTGCTTCGCGTTTGTACGTCCAGATGATGATGATGATGATGATGATGAT 1299

QY 401 GluProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProVal 420

Db 1300 GAGCCGCTGGTCCGTCGTCCTTGGTTAATGATCGGTTGTCCCGTCGATGGGTTCGGTT 1359

Qy 421 AspAlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSer 440

Db 1360 GATGCTTTGGGAGATGATCCCGGATAGCTTTGTGAGGGGTTGAGCTTTGTAGATCT 1419

Qy 441 GlyGlyAspTrpAlaGluCysPheAla 449

Db 1420 GGGGGTGAATTGGCGGAGTGTTTGTCT 1446

RESULT 3

ABN85591

ID ABN85591 standard; DNA; 1344 BP.

XX

AC ABN85591;

XX

DT 17-SEP-2002 (first entry)

XX

DE Aspergillus niger phyA related polynucleotide 4.

XX

KW Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; gene; ds.

XX

OS Aspergillus niger.

XX

PN CM133363-A.

XX

XX 30-JAN-2002.

PD

PF 12-JUL-2000; 2000CN-00117245.

XX

PR 12-JUL-2000; 2000CN-00117245.

XX

PA (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.

XX

PI Chen Z, Yang L, Fang L;

XX

DR WPI; 2002-305615/35.

XX

PT Phytase gene sequence and application in yeast thereof.

XX

PS Disclosure; Fig 5; 48pp; Chinese.

XX

CC The invention relates to a coded phytase gene sequence suitable for secretion and expression in yeast and its application. It is mainly characterized by removing nucleotide sequence of +45--+146 bit from phyA total length structure gene sequence, removing Aspergillus niger signal peptide coded sequence of +1--+44 and +147--+159, connecting a part of signal peptide code sequence suitable for secretion and expression at 5' end and connecting a restriction endonuclease site at 3' end. The different carriers can be connected into said gene sequence so as to form a recombinant plasmid with different functions and after the recombinant plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia yeast, finally the invented Pasteur Pichia yeast engineering bacterium (CCTCC NO:M200005) can be obtained through the screening process. By using the invention the industrial process of phytase bio-expression can be successfully implemented. The present sequence is that of a polynucleotide of the invention

XX

QQ Sequence 1344 BP; 286 A; 420 C; 329 G; 309 T; 0 U; 0 Other;

XX

Alignment Scores:

Pred. No.: 1.82e-234 Length: 1344

Score: 2353.00 Matches: 448

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 99.79% Indels: 0

DB: 6 Gaps: 0

US-10-089-364-4 (1-449) x ABN85591 (1-1344)

Qy 2 LeuAlaValProAlaSerArgAsnGlnSerCysAspThrValAspGlnGlyTyrGln 21

Db 1 CTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTCCGATAGGTCGATCAGGGGTATCAA 60

Qy 22 CysPheSerGlyThrSerHisLeuTrpGlyGlnTyrAlaProPheSerLeuAlaAsn 41

Db 61 TGTCTTCTCGAGACTTCGCATCTTTGGGTCATACGACACCGTCTTCTCTCTGCGCAAC 120

Qy 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61

Db 121 GAATCGGTTCATCTCCCTCAGGTGCGCGCGGATGCAGAGTCACCTTCGCTCAGGCTCTC 180

Qy 62 SerArgHisGlyAlaArgTyrProThrAspSerIleGlyIleValTyrSerAlaLeuIle 81

Db 181 TCCGTCATGAGCGCGCTATCCGACCGACTCCAGGGCAAGAAATACCTCCGCTCTCAT 240

Qy 82 GluGluIleGlnAsnAlaThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101

Db 241 GAGGAGATCCAGCAGAACCGGACCACTTTGAGGHAATATATGCTTCCTGAAGACATAC 300

Qy 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121

Db 301 AACTACAGCTTGGGTGCAGATGACCTGACTCTCCCTTCGGAGAACAGAGCTAGTCAACTCC 360

Qy 122 GlyIleIlePheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141

Db 361 GGCAATCAAGTTCTACCGAGCGGTACGAATCGCTCACAGGAACATCGTTCCATTCATCCGA 420

Qy 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161

Db 421 TCCCTCGGCTCCAGCGCGGTGATCGCTCGGGCAAGAAATTCATCGAGGGCTTCCAGAGC 480

Qy 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181

Db 481 ACCAAGCTGAAGGATCTCTCGTCCAGCGCCGCGCAATCGTCGCGCCAGATCGACGTGGTC 540

Qy 182 IleSerGluAlaSerSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201

Db 541 ATTTCCGAGGCCAGCTCATCCAAACACACTCTCGACCCAGCACCTGCACTGCTTCGAA 600

Qy 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221

Db 601 GACAGCGAATGGCCGATACCGTCGAGGCCAATTTACGCCCGACGTTCTGCTCCCTCAT 660

Qy 222 ArgGluArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241

Db 661 CGTCAACGCTCGAGAACGACCTGTCGCGTGTGACTCTCACAGACACAGAGTGAACCTAC 720

Qy 242 LeuMetAspVetCysSerPheAspThrIleSerThrThrValAspThrLysLeuSer 261

Db 721 CTATGGACATGTCTCTTCGACACCATCTCCACCGACACCCGTCGACACCAAGCTGTCC 780

Qy 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281

Db 781 CCCTTCGTGACCTGTTTCCCCATGAGATGGATCAACTACGACTACCTCCAGTCCCTTG 840

Qy 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301

Db 841 AAAAAATATTACGGCCCATGTGTGAGTAAACCGCTCGCGCCGACCCAGGGCGTGGGTAC 900

Qy 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321

Db 901 GCTAACGAGCTCATCGCCCGTCTGACCCACTCGGCTGTCCAGATGACACAGTCCACAC 960

Qy 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341

Db 961 CACACTTTGGACTCGACCGCGGTACCTTTCCGCTCAACTCTACTCTCTACCGCGACTTT 1020

Qy 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361

Db 1021 TCGCATGACACCGCATCATCTCCATTCCTTTTAGTCTGTGTATCAACGGCACATAAG 1080

Qy 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381

Db 1081 CCGCTATCTACACGACCGGTGGAGAAATATACCCACAGACAGATGATTCCTGCTGCTGG 1140

QY	2	LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln	21
Db	30	CTGGCAGTCCCAGCCTCTAGAATCAATCCTCTTGATCTGTCTGCATCAGGGTTATCAA	89
QY	22	CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn	41
Db	90	TGTTTCTCCGAGACTTCTCATCTTTGGGTCAATACGCACCATTTCTTCTCTGGCAAC	14
QY	42	GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu	61
Db	150	GAATCTGTCAITCTCCCTCAGGTGCACCGCATGTAGAGTCACTTTCCGCTCAGCTCCTT	20
QY	62	SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle	81
Db	210	TCCAGACATGGAGCTAGATATCCACCAGCTCCAGGGTAAGAAATATCTCGCTCTTATT	26
QY	82	GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr	10
Db	270	GAGGAGATCCAGCAGAACCTTACCACCTTTGACGGAAATATGCCTTCTCGAAGACATAC	32
QY	102	AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer	12
Db	330	MACTACTCTTTGGGTGCATGACCTGACTCCATTCGGAGAACAGGAGCTTGTCACTCC	38
QY	122	GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg	14
Db	390	GGTATCAAGTTCTACAGAGATACGAATCTTTGACAGAAACATCGTTCCATTTCATCAGA	44
QY	142	SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer	16
Db	450	TCTCTGGTTCTCTAGAGTTATCGCCTCCGGTAAGAAATTCATCGAGGGTTTCCAGAGC	50
QY	162	ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal	18
Db	510	ACTAAGTCGAAGATCCTTAGAGCCAGCCAGTCAATCTTCTCCAAAGATCGAGTTGTC	56
QY	182	IleSerGluAlaSerSerSerAsnAsnThrIleuAspProGlyThrCysThrValPheGlu	20
Db	570	ATTTCCGAGGCCTCTTCTATCCAAACAACTCTTGACCCAGGTACTGTACTGTCTTCGAA	62
QY	202	AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle	22
Db	630	GACTCTGATTTGGCCGATCTGTGCAAGCCAAATTCCTGCACTTTCTGCTCCCATCCATT	68
QY	222	ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr	24
Db	690	AGACAAAGACTGGAGAACGACCTGTCCGGTGTACTCTTACTGACACTGAAGTACTTAC	74
QY	242	LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer	26
Db	750	CTTATGGACATGTGTCTCTTGACACTATCTCCACTTCTACCGTGCACACCAAGCTGTCC	80
QY	262	ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu	28
Db	810	CCATCTCTGTGACCTGTTCAACCATGACGATGGATCAACTACGACTACTTTCGAGTCTCTG	86
QY	282	LysLysTyrTyrGlyHisGlyAlaGlyAsnProIleuGlyProThrGlnGlyValGlyTyr	30
Db	870	AAAAAGTATTACGGTCATGGTGCAGGTAAACCATTTGGGTCCAAACCCAGGGTGTCCGTTAC	92
QY	302	AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn	32
Db	930	GCTAACGAGTTGATGCCAGACTGACCCACTCTCTCTGTCCAGATGATGACCTCTTCCAAC	98
QY	322	HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe	34
Db	990	CACACTTTGGACTCTTCTCCAGTACCTTTCATTGAACCTACTCTTGTACGCTGACTTT	104
QY	342	SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys	36

Alignment Scores:	
Pred. No.:	1.9e-234
Score:	2353.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	99.79%
DB:	6
	Gaps:
	0
	Indels:
	0
	Mismatches:
	0
	Conservative:
	0
Matches:	448
Length:	1382

Db 1050 TCTCATGACACAGGTATCATCTCCATTTTGGTTGGCTTTAGTCTGTGTACAAACGGTACTAAG 1109
 QY 362 ProLeuSerThrThrValGluAlaSerArgLeuValGluMetMetGlnCysGlnAlaGluGlnGlu 381
 Db 1110 CCATTGCTTACCACTACCGTGTGAGATATACCCACAGACAGATGGATTCTCTCTGCTTGG 1169
 QY 382 ThrValProPheAlaSerArgLeuValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 Db 1170 ACUTGTTCCATTGCTTCTAGATTGTACGTGAGATGATGAGTGTGAGCTGAGCAGAG 1229
 QY 402 ProLeuValArgValLeuValAlaSerArgValValProLeuHisGlyCysProValAsp 421
 Db 1230 CCACCTGGTCAGAGTCTTGGTTAATGATAGATTGTCCCACTGCATGGTTGCTGTGTAT 1289
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSergly 441
 Db 1290 GCTTTGGGTAGATGTACCAAGATTCTTTGTTAGAGGTTTGTCTTTGCTAGATCTGTT 1349
 QY 442 GlyAspTIPAlaGluCysPheAla 449
 Db 1350 GGTGATGGGTGAGTGTGTGCT 1373

RESULT 5

ID ABN85590
 ID ABN85590 standard; DNA; 1389 BP.

AC ABN85590;

XX 17-SEP-2002 (first entry)

DE Aspergillus niger phyA related polynucleotide 3.

XX Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; gene; ds.

OS Aspergillus niger.

FH Key Location/Qualifiers
 CD 1..1347

FT /*tag= a

FT /product= "phyA related protein"

XX CN1333363-A.

XX 30-JAN-2002.

XX 12-JUL-2000; 2000CN-00117245.

XX 12-JUL-2000; 2000CN-00117245.

XX (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.

XX Chen Z, Yang L, Fang L;

XX WPI; 2002-305615/35.

XX P-PSDB; ABB83811.

XX Phytase gene sequence and application in yeast thereof.

XX Disclosure; Fig 4; 48pp; Chinese.

CC The invention relates to a coded phytase gene sequence suitable for
 CC secretion and expression in yeast and its application. It is mainly
 CC characterised by removing nucleotide sequence of +45-+146 bit from phyA
 CC total length structure gene sequence, removing Aspergillus niger signal
 CC peptide coded sequence of +1-+44 and +147-+159, connecting a part of
 CC signal peptide code sequence suitable for secretion and expression at 5'
 CC end and connecting a restriction endonuclease site at 3' end. The
 CC different carriers can be connected into said gene sequence so as to form
 CC a recombinant plasmid with different functions and after the recombinant
 CC plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia
 CC yeast, finally the invented Pasteur Pichia yeast engineering bacterium
 CC (CCTCC NO:IM200005) can be obtained through the screening process. By
 CC using the invention the industrial process of phytase bio-expression can

CC be successfully implemented. The present sequence is that of a
 CC polynucleotide of the invention

SQ Sequence 1389 BP; 332 A; 362 C; 293 G; 402 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.91e-234 Length: 1389
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 6 Gaps: 0

US-10-089-364-4 (1-449) X ABN85590 (1-1389)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 Db 31 CTGGCAGTCCCAGCCCTCTAGAAATCAATCCTCTTGTGATACTGTGATCAGGGTTATCAA 90
 QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 Db 91 TGTTCCTCCGAGACTTCTCATCTTTGGGGTCAATACGCACCATTTCTTCTCTGGCAAC 150
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 151 GAATCTGTCTATCTCCCTGAGGTGCCAGCGGATGTAGATCACTTTCGTCAAGTCTT 210
 QY 62 SerArgHisGlyAlaArgTyrProThrAsnSerLysGlyLysLysTyrSerAlaLeuIle 81
 Db 211 TCCAGACTGGAGCTAGATATCCACCGACTCCAGGGTAAGAAATACCTCCGCTCTTATT 270
 QY 82 GluGluIleGlnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 271 GAGGAGATCCAGCAGAACGCTACCACTTTGACGGAAATATGCTTCTCTGAAGACATAC 330
 QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
 Db 331 AACTACTCTTTGGGTGCAGATGACCTGACTCCATTCGGAGAACAGAGGCTTGTCAACTCC 390
 QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 391 GGATCAAGTTCTACCAGAGATACGAATCTTTGACAGAAACATCGTTCATTCATCAGA 450
 QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 451 TCCTCTGGTTCCTCTAGAGTTATCGCTCCGGTAAGAAATTCATCAGAGGTTTCCAGAGC 510
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 Db 511 ACTAAGCTGAAGGATCTAGAGCCAGCCAGGTCATCTTCTCCAAAGATCGAGCTTGTTC 570
 QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 Db 571 ATTTCCGAGGCCCTCTTCAUCCAAACACACTTTGACCCAGTACTGTACTGTCTTCGAA 630
 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 Db 631 GACTCTGAATTTGCCGATACTGTGGAAGCCAAATTCATGCCACTTTCGTCCTCCATCAT 690
 QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 Db 691 AGACAAGACTGGAGAACGACCTGTCCGGTGTGTACTTCTACTGACACTGAAGTTACTTAC 750
 QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
 Db 751 CTTATGACAGATGTTCTCTCGACACTATCTCCACTTCTACCGTCGACACCAAGCTCTCC 810
 QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 811 CCATTCGTGACCTGTTCACCCATGACGAATGGATCAACTACGACTACTTTCGAGTCTCTTG 870
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301

Db 871 AAAAGATATTACGGTCATCGTCAGGTAACCCCATTTGGTCCACACCGAGGTGTGCGTTAC 930
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 931 GCTAAGAGTTGATCCGAGAGTACCCACTCTCTGTCACGATGACACCTCTTCCAAC 990
 QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 Db 991 CACACTTTGGACTCTCTCCAGCTACCTTCCATTGAACCTACTTTGTAGCGTGACTTT 1050
 QY 342 SerHisAspAsnGlyIleLeuSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 Db 1051 TCTCAGACAAACGGTATCATCTCCATTTTGTTCCTTTAGGCTGTACAAACGGTACTAAG 1110
 QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
 Db 1111 CATTGTCTACCACTACCGTTGAGATATACCCAGACAGATGGATCTCTTCTGCTTGG 1170
 QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 Db 1171 ACTGTTCCATTTGCTTCTAGATTGTACGTCGAGATGATCGAGTCTCAGGCTGAGCAGGAG 1230
 QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 Db 1231 CCACCTGGTCAGAGTCTTGGTTAATGATAGAGTTGTCCCACTGCATGTTGTCTGTGAT 1290
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 1291 GCTTGGGTAGATGATACAGAGATCTTTTGTAGAGTTTGTCTTTTCTAGATCTGTT 1350
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 Db 1351 GGTGATTGGGCTGAGTGTCTTGTCT 1374
 RESULT 6
 ID AAQ11175 standard; cDNA; 1404 BP.
 XX AC AAQ11175;
 DT 25-MAR-2003 (revised)
 DT 30-MAR-2000 (revised)
 DT 31-MAY-1991 (first entry)
 XX Chromosomal phytase encoding sequence.
 DE Microbial phytase; animal feed; inositol; inorganic phosphate; ss.
 KW Synthetic.
 OS
 FH Key Location/Qualifiers
 CDS 1..1404
 FT /*tag= a
 FT /product= "chromosomal phytase"
 FT sig_peptide 1..69
 FT /*tag= b
 PN EP420358-A.
 XX
 PD 03-APR-1991.
 XX
 PF 27-SEP-1990; 90EP-00202565.
 XX
 PR 27-SEP-1989; 89EP-00202436.
 PR 17-AUG-1990; 90EP-00202231.
 XX
 FA (KONN) GIST-BROCADES NV.
 FA (STAM) DSM NV.
 XX
 PI Van Gorcom RF, Van Hartingsveldt W, Vanparidon PA, Beenstra AE;
 PI Luiten RG, Selden GCM;
 XX
 DR WPI; 1991-095799/14.

P-PSDB; AAR11333.

XX DNA encoding phytase - used for recombinant expression for prodn. of
 PT phytase for conversion of phytate to inositol and inorganic phosphate
 FT esp. in animal feed.
 XX

Disclosure; Fig 8; 61pp; English.

XX This sequence is the translation region deduced from comparisons of
 CC respective sequences of clones identified using oligonucleotide probes.
 CC The use of recombinant DNA methods for the enzyme prodn. allows the
 CC large scale prodn. of proteins and peptides having phytase activity.
 CC These are used for the conversion of phytate to inositol and inorganic
 CC phosphate and can be used in industrial processes. The phosphate content
 CC of manure thus can be decreased. See also AAQ11157-74. (Revised record
 CC issued to correct errors present in the sequence portion of the original
 CC GENESBQ entry.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on
 CC 25-MAR-2003 to correct PI field.)
 XX

SQ Sequence 1404 BP; 293 A; 436 C; 344 G; 331 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.94e-234 Length: 1404
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 2 Gaps: 0

US-10-089-364-4 (1-449) x AAQ11175 (1-1404)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 Db 58 CTGGCAGTCCCGCGCTCGAGAAATCAATCCAGTTTSCGATACGTCGATCAGGGGTATCAA 117
 QY 22 CysPheSerGluThrSerHisLeuTyrGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 Db 118 TGTCTCTCCGAGACTTCGCATCTTTGGGGTCAATACGACACCGTCTTCTCTCTGGCAAC 177
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 178 GAATCGGTCACTCCCTGAGTGCCCGCGGATGTCAGAGTCACATTCGCTCAGTCTCTC 237
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
 Db 238 TCCCGTCAAGGAGCGCGGTATCCGACCGACTCCAGGGCAAGAAATACCTCCGCTCAT 297
 QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 298 GAGGAGATCCAGCAGAGACGCGACCCCTTTGACGGAAATATGCTTCTCTGAAGACATAC 357
 QY 102 AsnTyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
 Db 358 AACTACAGCTTGGGTGCAGATGACTGACTCCCTTCGGAGAACAGGAGCTAGTCAACTCC 417
 QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 418 GGCATCAAGTTCTACCGCGGTACGAATCGCTCAAGGAACATCGTTCCATTATCCGA 477
 QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 478 TCCTCTGGCTCCAGCCGGGTGATCGCTCCGGCAAGAAATTCATCGAGGGGTTCAGAGC 537
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 Db 538 ACCAAGCTGAAGGATCCTCGTCCCGCAGCCGCGCAATCGTCCGCCAAGATGACGCTGTC 597
 QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 Db 598 ATTTCCGAGGCCAGCTCATCCAAACACTCTCCAGCCAGGACCTGCTGCTTCTCGAA 657
 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221

Db 658 GACAGCGAATTGGCCGATACCGTTCGAAGCAATTTTCAACGCCACGCTTCGTCCTCCAT 717
 QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 Db 718 CGTCAACGCTGTGAGAACGACCTGTCCGGTGTGACTCTCACGACACAGAAGTGACTAC 777
 QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrValAspThrLysLeuSer 261
 Db 778 CTATGGACATGTGCTTCGACACCACTCCACGACACCGCTGCACACCAAGCTGTCC 837
 QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 838 CCCTTCTGTGACCTGTTCACCCATGACGAATGATCAACTACGACTACCTCCAGTCTCTG 897
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 898 AAAAAGTATTACGCCCATGTGTGAGGTAAACCGCTCGGCCCGACCGGGCGTGGCTAC 957
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 958 GCTAACAGACTCATCGCCCTGTGACCCACTCGCCTGTCCACGATGACACCACTCCAAC 1017
 QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 Db 1018 CACACTTTGGACACGAGCCCGGTACCTTTCGGCTCAACTCTACTCTCTACGGCGACTTT 1077
 QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 Db 1078 TCGCATGACAAACGGCATCATCTCCATCTCTTGTCTTGGTCTGTACACGGCACCTPAG 1137
 QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
 Db 1138 CCGCTATCTACACGACCGGTGGAGAAATATACCCAGACAGATGGATTCTCGTCTGCTGG 1197
 QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetGlnCysGlnAlaGluGlnGlu 401
 Db 1198 ACGGTTCCGTTTGGCTTCGCGTTTGTACGTCGAGATGATGAGTGTACAGCGGAGCAGGAG 1257
 QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 Db 1258 CCGCTGTGTCCGTGCTTGTGGTTAATGATCGCGTGTGTCCTCCGCTGCATGGGTGTGAT 1317
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 1318 GCTTTGGGAGATGTACCCGGATAGCTTTGTGAGGGGTTGACCTTTGTAGATCTGGG 1377
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 Db 1378 GGTGATTGGCGGAGTGTGTTTGCT 1401
 RESULT 7
 ID AA227421
 AC AA227421;
 XX
 XX
 DT 27-AUG-2003 (revised)
 DT 07-DEC-1999 (first entry)
 XX
 XX
 DE A. ficum phytase coding sequence.
 XX
 KW Phytase; variant; enzyme; phosphorus liberation; phytase substrate;
 KW phytate level reduction; animal manure; food preparation; soy processing;
 KW inositol manufacture; ss.
 XX
 OS Aspergillus ficum.
 XX
 XX
 FN WO9949022-A1.
 XX
 XX
 PD 30-SEP-1999.
 XX
 XX
 PF 22-MAR-1999; 99WO-DK000153.
 XX
 XX

PR 23-MAR-1998; 98DK-00000407.
 PR 19-JUN-1998; 98DK-00000806.
 PR 18-SEP-1998; 98DK-00001176.
 PR 22-JAN-1999; 99DK-00000091.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 XX
 XX Svendsen A;
 PI
 XX
 XX WPI; 1999-580444/49.
 DR F-PSDB; AAY39904.
 XX
 XX
 PT
 PT
 PT
 PT
 PS Disclosure; Fig 11; 141pp; English.
 XX
 CC This sequence encodes the Aspergillus ficum phytase sequence. The
 CC invention relates to variant phytase enzymes with specific amino acid
 CC substitutions for improved properties. The phytase variants can be used
 CC for liberating phosphorus from a phytase substrate. They can be used for
 CC reducing phytate levels in animal manure. They can be used in feed or
 CC food preparations. The phytase DNA can also be used to produce transgenic
 CC plants which can be used in feeds or foods. The phytase variants can also
 CC be used in soy processing and in the manufacture of inositol or
 CC derivatives. The phytase variants can have altered activities such as pH
 CC stability, temperature stability, pH profile, temperature profile,
 CC specific activity (in particular in relation to pH and temperature),
 CC substrate specificity, substrate cleavage pattern, substrate binding,
 CC position specificity, the velocity and level of release of phosphate from
 CC corn, reaction rate, phytase degradation rate and end level of released
 CC phosphate reached. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 1404 BP; 293 A; 436 C; 344 G; 331 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,94e-234 Length: 1404
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 2 Gaps: 0

US-10-089-364-4 (1-449) x AA227421 (1-1404)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerCysAspThrValAspGlnGlyTyrGln 21
 Db 58 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGTCGATCGGGGTATCAA 117
 QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 Db 118 TGCTTCTCCGAGACTTCGCATCTTTGGGTCAATACGACCGCTTCTCTCTGGCAAC 177
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 178 GAATCGGTCTATCTCCCTCGAGTCCCGCGGATGACAGAGTCACTTTCGCTCAGTCTC 237
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
 Db 238 TCCGCTCATGGACCGCGGTATCCGACGACTCCCAAGGGCAAGAAATATCCGCTCAT 297
 QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 298 GAGGAGATCCAGCAGAACCGCACCATCTTTGACGAAAAATATGCTCTCTCTGAAGACATAC 357
 QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
 Db 358 AACTACAGCTTGGGTGAGATGACTGACTCCCTTCGGAGAACAGGAGCTAGTCACTCC 417
 QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 418 GGCATCAAGTTCTACCGACGCTACGATCGCTCACAGGAACATCGTTCCTCATTCGCA 477

QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 478 TCCTCTGGCTCCAGCGCGTGTGCTCGCCGACGAATTCATCGAGGCTTCAGAGC 537
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 Db 538 ACCAAGCTGAGGATCTCGTCCAGCGCGGCAATCGTCGCCAAGATCGACGTGGTC 597
 QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 Db 598 ATTTCGAGGCGGAGCTCAFCACCAACACTCTCGACCCAGGACCTGCACTCTCTTCGAA 657
 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 Db 658 GACACGGAATTGGCCGATACCTCGAGCAATTCACCGCCACGTTCTGTCCTCCAT 717
 QY 222 ArgGlnArgLeuGluAlaAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 Db 718 CGTCAACGCTCGAGAACGACCTGTCGGTGTGACTCTCACAGACACAGAAGTGACCTAC 777
 QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrValAspThrLysLeuSer 261
 Db 778 CTCATGGACATGCTCTCTTCACCAACCACTCCACGACCGCTCGACCAAGCTGTCC 837
 QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 838 CCCTTCTGTGACCTGTTCCACCATGACGAATGATCACTACGACTACTCTCCAGTCTCTTG 897
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 898 AAAAAGTATTACGGCCATGTCAGTAACTCCGCTCGGCCCGACCGGCGTCGGCTAC 957
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 958 GCTACGAGCTCATCGCCGCTGACCACTCGCTGTCCAGATGACCAAGTTCACAC 1017
 QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 Db 1018 CACACTTTGGACTCGAGCGCGGTACTTTTCGCTCACTCTACTCTCTACGGGACTTT 1077
 QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 Db 1078 TCGCATGACAAAGGATCATCTCTCTCTTTAGTCTCTACACGGCACTAAG 1137
 QY 362 ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
 Db 1138 CCGCTATCTACCAACCGGTGGAGAAATATCAACAGACAGATGGATCTCGTCTGCTGG 1197
 QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 Db 1198 ACGGTTCGGTTTGTCTCGGTTGTACGTCGAGATGATCGAGTGTACGGGAGCAGAG 1257
 QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 Db 1258 CCGTGTGTCCTGTCTGTGTTAACTATCGCTGTGTCGCTGTCATGGGTTCAT 1317
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 1318 GCTTTGGGAGATGATACCGGGATAGCTTTGTGAGGGGTTGTAGCTTTGTAGATCTGGG 1377
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 Db 1378 GGTGATCGGGAGTGTGTGCT 1401

RESULT 8

ABN85588
 ID ABN85588 standard; DNA; 1506 bp.

XX AC ABN85588;

XX 17-SEP-2002 (first entry)

DT

DE Aspergillus niger phyA related polynucleotide 2.
 KW Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; gene; ds.
 XX Aspergillus niger.
 OS
 FH Key Location/Qualifiers
 CDS 1..1506
 FT /*tag= a
 FT /product= "phyA related protein"
 FT 1..44 /*tag= b
 FT /number= 1
 FT 45..146 /*tag= c
 FT /number= 1
 FT 147..1506 /*tag= d
 FT /number= 2
 XX
 PN CN1333363-A.
 XX
 PD 30-JAN-2002.
 XX
 PF 12-JUL-2000; 2000CN-00117245.
 XX
 PR 12-JUL-2000; 2000CN-00117245.
 XX
 PA (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.
 XX
 PI Chen Z, Yang L, Fang L;
 XX
 DR WPI: 2002-305615/35.
 DR P-PSDB; ABE83810.
 XX
 PT Phytase gene sequence and application in yeast thereof.
 XX
 PS Disclosure; Fig 1; 48pp; Chinese.
 XX
 CC The invention relates to a coded phytase gene sequence suitable for secretion and expression in yeast and its application. It is mainly characterised by removing nucleotide sequence of +45-+146 bit from phyA total length structure gene sequence, removing Aspergillus niger signal peptide coded sequence of +1-+44 and +147-+159, connecting a part of 5' signal peptide code sequence suitable for secretion and expression at 5' end and connecting a restriction endonuclease site at 3' end. The different carriers can be connected into said gene sequence so as to form a recombinant plasmid with different functions and after the recombinant plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia yeast, finally the invented Pasteur Pichia yeast engineering bacterium (CTCC NO:M200005) can be obtained through the screening process. By using the invention the industrial process of phytase bio-expression can be successfully implemented. The present sequence is that of a polynucleotide of the invention
 XX
 SQ Sequence 1506 BP; 318 A; 465 C; 369 G; 354 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2.15e-234 Length: 1506
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 6 Gaps: 0

US-10-089-364-4 (1-449) x ABN85588 (1-1506)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 Db 160 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGTCGATCGGGTATCAA 219
 QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 DT

Db 220 TGCCTTCGCGAGCTTCGCATCTTTGGGGTCAATACGACCGCTTCTCTCTCTGCGCAAC 279
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValIleu 61
 Db 280 GAATCGGTTCATCTCCCTCAGGTGCGCGCGATGCGAGTCACTTTCCTCAGGTCCTC 339
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
 Db 340 TCCCGTCATGGAGCGCGGTATCCGACCGACTCCAGGGCAAGAAATCTCCGCTCTCAT 399
 QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 401
 Db 400 GAGGAGATCCAGCAGAACGCGACCACTTTGACGGAAATATGCTTCTCTGAAGACATAC 459
 QY 102 AsnTyrSerIleuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
 Db 460 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGGAACAGAGCTAGTCACTCC 519
 QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 520 GGCATCAAGTTCACGACGGGTACGATCGCTCAAGGACATCGTTCATTCATCCGA 579
 QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 580 TCCTCTGGCTCCAGCGCGGTATCGCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGC 639
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 191
 Db 640 ACCAAGCTGAAGGATCTCTCGTCCGACCGCGGCAATCGTCCGCAAGATCGACGTGGTC 699
 QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 Db 700 ATTTCCGAGCCAGCTCATCCACACACACTCTCGACCCAGGACCTGCATCTGCTTCGA 759
 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 Db 760 GACAGCGAATTTGGCCGATACCGTCCGAAGCCAAITTCACCGCCACGTTCCGTCCTCCAT 819
 QY 222 ArgGlnArgIleuGluAsnAspLeuSerGlyValThrIleuThrAspThrGluValThrTyr 241
 Db 820 CGTCAACGCTTGAGACGACGCTCGCGGTGACTCTCACACACACAGAGTGACCTAC 879
 QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
 Db 880 CTATGACATGTGCTCTCTCGACACATCTCCACGACGACCGTCCGACACCAAGCTGCC 939
 QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 940 CCTTCTGTGACCTGTTCACCCATGACGAATGGATCAACTACGACTACCTCCAGTCCCTTG 999
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 1000 AAAAAGPATTACGGCCATGTGCGAGTAAACCGCTCGGCCCGACCCAGGCGTCCGGTAC 1059
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 1060 GCTAACGAGCTCATCGCCCGCTCTCACCACTCGCTCTCCAGATGACACAGTTCACAC 1119
 QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 Db 1120 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1179
 QY 342 SerHisAspAsnGlyIleIleSerIlePheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 Db 1180 TCGCATGACACCGCATCATCTCTCTCTTTAGTCTGTATGATACAGCGCACATAG 1239
 QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
 Db 1240 CCGTATCTACACGACCGTGGAGATATACCCAGACAGATGATTCGTCTGCTGTGG 1299
 QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 Db 1300 ACGGTTCCGTTTGTCTCGCGTTTGTACGTCGAGATGATGCAGTGTCAAGCGGACGAGAG 1359

QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 Db 1360 CCGCTGGTCCGTGCTTGTGTTAATGATCGGCTGTCATGGGTGTCGCGTTGAT 1419
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 1420 GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTCTAGATCTGG 1479
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 Db 1480 GGTGATTTGGCGGAGTGTTTTGCT 1503

RESULT 9

ID ADL91241 standard; DNA; 2665 BP.
 AC ADL91241;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Wild-type phytase coding sequence, SEQ ID 1.
 XX
 KW Phytase; enzyme; foodstuff; animal feed; inositol phosphate; gene; ds.
 XX
 OS Aspergillus niger.
 XX
 PN WO2004024885-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 15-SEP-2003; 2003WO-US028923.
 XX
 PR 13-SEP-2002; 2002US-0410736P.
 XX
 PA (CORR) CORNELL RES FOUND INC.
 PA (USDA) US SEC OF AGRIC.
 XX
 PI Lei X, Mullaney EJ, Ullah AHJ;
 XX
 DR WFI; 2004-270029/25.
 DR P-PSDB; ADL91242.

Novel isolated mutant phytase e.g. PhYA useful for feeding monogastric animals, improving nutritional value of foodstuffs consumed by animal, in vitro hydrolysis of phytate or improving nutritional value of foodstuffs consumed by humans.

Disclosure; SEQ ID NO 1; 215pp; English.

The present invention relates to mutant phytases (I) and their coding sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309). (I) have altered pH profiles and altered pH optima compared to a corresponding non-mutant phytase. (I) are useful for improving the nutritional value of a foodstuff which involves providing a foodstuff comprising myo-inositol hexakisphosphate, providing (I) and feeding to the animal the foodstuff in combination with (I) under conditions effective to increase the bioavailability of phosphate from phytate. (I) are also useful for feeding a monogastric animal (e.g., fowl species, porcine species, aquatic species, domestic animal chosen from canine species and a feline species, or mammalian species chosen from *Oryctolagus*, *Capra*, *Bos*, *Equus* and *Ovis* species) which involves feeding foodstuff in combination with (I), to the animal. (I) are also useful for producing specific inositol phosphate metabolites or products for nutritional and biomedical applications. The present sequence is a wild-type phytase coding sequence, which was used to produce the mutants of the invention.

Sequence 2665 BP; 633 A; 808 C; 574 G; 650 T; 0 U; 0 Other;

Alignment Scores: 4.98e-234 Length: 2665
 Pred. No.: 2353.00 Matches: 448
 Score:

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 12 Gaps: 0

US-10-089-364-4 (1-449) x ADL91241 (1-2665)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 DB 842 CTGGAGTCCCGCTCGAGAAATCAATCAGTTGGATACGGTCAATCAGGGGTATCAA 901

QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 DB 902 TGCCTCTCCGAGACTCGCATCTTTGGGTCAATACGCACCGCTTCTCTCTCGGCAAC 961

QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 DB 962 GAATCGGTCACTCCCTCAGGTGCCCGCGGATCGAGTCACTTTCCGCTCAGGTCTTC 1021

QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
 DB 1022 TCCCGTCAITGAGCGCGGTATCCGACCGACTCCAGGGCAAGAAATACTCCGCTCTCAT 1081

QY 82 GluGluIleGlnIleAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 DB 1082 GAGGAGATCCACAGACGCGACCACTTTTGCGGAAATATGCCCTTCTCGAAGCAATAC 1141

QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluValAsnSer 121
 DB 1142 AACTACAGCTGGGTGAGATGACTGCTCCCTTCGGGAGAACAGGAGCTAGTCAACTCC 1201

QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 DB 1202 GGCATCAAGTTCTACAGCGGTACGAATCGCTCACAGGAACATCGTTCATTCGCA 1261

QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 DB 1262 TCCTCTGCTCCAGCGGTGATCGCTCCCGCAAGAAATTCATCGAGGGCTTCAGAGC 1321

QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 DB 1322 ACCAAGCTGAGAGATCTTCGTGCCCGCGCCCAATCGTGCCCAAGATCGACGTGTC 1381

QY 182 IleSerGluAlaSerSerSerAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 DB 1382 ATTTCCGAGGCCAGCTCATCAACAACACTCTCGACCCAGGACCTGCACTGTCTCGAA 1441

QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 DB 1442 GACAGCGAATTGGCGGATACCGTCAAGCCCAATTTACCGCCCACTGCTCCCTCCATT 1501

QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 DB 1502 CGTCAAGCTCTGGAGACAGACTGTGCGGTGAGCTCTCACAGACACAGAAAGTGACCTAC 1561

QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
 DB 1562 CTCATGGACATGTGCTCTTCGACACCATCTCCACAGACCGTCCGACCAAGCTGTCC 1621

QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 DB 1622 CCCTTCTGTGACCTGTTCCCGCATGACGAATGATCAACTACGACTCCAGTCCCTG 1681

QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 DB 1682 AAAAAGTATTACGCCCATGTGGTGCAGTAACCCGCTCGGCCCGACCCAGGGCGTCCGTAC 1741

QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 DB 1742 GCTAACGAGCTCATGCCCGTCTGACCACTCGCTGTCCAGATGACACCAAGTTCACAC 1801

QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341

DB 1802 CACACTTTGGACTCGAGCCCGCTACTCTTCGCTCAACTCTACTCTCTACGGGACTTT 1861

QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361

DB 1862 TCGCATGACACAGCATCATCTCCATTCTCTTTGCTTTAGGTCTGTACCAACGCACTAAG 1921

QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381

DB 1922 CGCTATCTACACAGCCGCTGGAGAAATATCACCCAGACAGATGGATCTCTGCTGCTGG 1981

QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401

DB 1982 ACGGTTCCGTTGCTTCGCTTGTACGTCGAGATGATGCACTGTCCAGCGGAGCAGGAG 2041

QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421

DB 2042 CGCTGGTCCGCTGTCTGTTAATGATCGCTGTCCGCTGCATGGGTGTCCGGTTGAT 2101

QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441

DB 2102 GCTTTGGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGACTGGG 2161

QY 442 GlyAspTrpAlaGluCysPheAla 449

DB 2162 GGTGATTGGGGAGTGTGTTGCT 2185

RESULT 10

AAQ11174
 ID AAQ11174 standard; DNA; 6756 BP.

XX AAQ11174;

XX 25-MAR-2003 (revised)

DT 31-MAY-1991 (first entry)

XX Sequence, from overlapping clones, encoding chromosomal phytase.

XX Microbial phytase; animal feeds; inositol; inorganic phosphates; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT CDS 210..1715

FT /*tag= b

FT /product= "chromosomal phytase"

FT intron 254..355

FT /*tag= a

XX EP420358-A.

XX 03-APR-1991.

XX 27-SEP-1990; 90EP-00202565.

XX 27-SEP-1989; 89EP-00202436.

XX 17-AUG-1990; 90EP-00202231.

XX (KONN) GIST-BROCADES NV.

XX (STAM) DSM NV.

XX Van Gorcom RF, Van Hartingsveldt W, Vanparidon PA, Beenstra AE;

XX Luiten RG, Selden GCM;

XX WPI; 1991-095799/14.

XX DNA encoding phytase - used for recombinant expression for prodn. of

XX phytase for conversion of phytate to inositol and inorganic phosphate

XX esp. in animal feed.

XX Disclosure; Page 32; 61pp; English.

XX

CC This sequence is a compilation of the respective sequences of clones pAF
 2-3, pAF 2-6 and pAF 2-7 identified using oligonucleotide probes. The use

CC of recombinant DNA methods for the the enzyme prodn. allows the large
 CC scale prodn. of proteins and peptides having phytase activity. These are
 CC used for the conversion of phytate to inositol and inorganic phosphate
 CC and can be used in industrial processes. The phosphate content of manure
 CC thus can be decreased. See also AAQ11157-73 and AAQ11175. (Updated on 25-
 CC MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
 CC field.)
 XX
 SQ Sequence 6756 BP; 1615 A; 1718 C; 1707 G; 1716 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1-96e-233 Length: 6756
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 2 Gaps: 0

US-10-089-364-4 (1-449) x AAQ11174 (1-6756)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 DB 369 CTGGCAGTCCCGCCCTCGAATAATCAATCCAGTTGGGATACGGTCGATACAGGGGTATCAA 428
 QY 22 CysPheSerGluThrSerHisLeuTyrGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 DB 429 TGGTTCCTCCGAGACTTCGCACTCTTGGGGTCAATACGCACCGTCTCTCTCTGGCAAC 488
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 DB 489 GAATCGGTATCTCCCTGAGGTGCGCGCGGATGCAGATCACTTTCGCTCAGGTCTCTC 548
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerIysGlyIysIysTyrSerAlaLeuIle 81
 DB 549 TCCCGTCATGAGCGCGGTATCCGACCGACTCCCAAGGGCAAGAAATACTCCGCTCTCAT 608
 QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyIysTyrAlaPheLeuIysThrTyr 101
 DB 609 GAGGAGATCCAGCAAGACGCGACCACTTTGACGGAAATATGCCITTCCTGAACATAC 668
 QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
 DB 669 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGAGGAGTACTCACTCC 728
 QY 122 GlyTleIysPheTyrGlnArgTyrGluSerLeuThrArgGlnIleValProPheIleArg 141
 DB 729 GGCATCAAGTCTTCAACGCGGTAGCAATCGCTCAAGGAACATPCGTTCATTCATCCGA 789
 QY 142 SerSerGlySerSerArgValIleAlaSerGlyIysIysPheIleGluGlyPheGlnSer 161
 DB 789 TCCTCTGGCTCCAGCCCGGTGATCGCTTCGGCAAGAAATTCATCGAGGGGCTCCAGAGC 848
 QY 162 ThrIysLeuIysAspProArgAlaGlnProGlyGlnSerSerProIysIleAspValVal 181
 DB 849 ACCAAGCTGAAGGATCCTCGTCCCGCAGCCCGCCCAATCGTCGCCCAAGATCGAGTGTCTC 908
 QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 DB 909 ATTTCCGAGGCCAGCTCATCCAAACACACTCTCCAGCCAGGACCTGACACGTCTTCGAA 969
 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 DB 969 GACAGCGAATTGGCCGATACCGTCGAGGCCAATTTACCGCCGACGTTCTGCTCCCTCCAT 1028
 QY 222 ArgGlnArgLeuGluAlaAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 DB 1029 CGTCAACGCTCTGGAGAACGACTCTCGCGTGTGATCTCTCACAGACACAGAGTACCTAC 1088
 QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrIysLeuSer 261
 DB 1089 CTCATGGACATGTGCTCTTCGACACCATCTCTCCACGACCGCTCGACACCAAGCTGTCC 1148
 QY 262 PropheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281

DB 1149 CCCTTCTGTGACCTGTTCACCATGACGAATGATCAACTACGACTACCTCCAGTCCCTTG 1208
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 DB 1209 AAAAGATATTACGGCATGGTCAGGTAAACCGCTCGGCCGCCAGCCGCGCTCGGCTAC 1268
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 DB 1269 GCTAACGAGCTCATCGCCGCTGTGACCCACTGCGCTGTCCACGATGACACCACTTCCAAC 1328
 QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 DB 1329 CACACTTTGGACTCGAGCCCGCTACCTTTCCGCTCACTCTCTACGCGGACTTT 1388
 QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 DB 1389 TCGCATGACAAACGGCATCATCTCCATCTCTTTGCTTTAGTCTGTACACGCGACTAAG 1448
 QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
 DB 1449 CCGCTATCTACACGACCGGTGGAGATATCACCCAGACAGATGGATTCTCGTCTGTGG 1508
 QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 DB 1509 ACGGTTCCGTTTCTCGGCTTTGTACGTGAGATGTCAGTGTGAGCGGAGCAGGAG 1568
 QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 DB 1569 CCCTGCTCGCTGCTGTGGTTAATGATCGCGTGTCCCGCTGATGGGTGTCCGGTTGAT 1628
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 DB 1629 GCTTTGGGAGATGATCCCGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 1688
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 DB 1689 GGTGATTGGCGGAGTGTGTTGCT 1712

RESULT 11
 AAT65137 standard; cDNA; 6756 BP.
 ID AAT65137
 XX AC AAT65137;
 XX DT 17-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 21-AUG-1997 (first entry)
 XX DE Aspergillus ficuum phytase genomic DNA.
 XX KW Phytase; phytate; inositol; animal feed; ss.
 XX OS Aspergillus ficuum; NRRL 3135.
 XX PH Key Location/Qualifiers
 FT primer_bind /*tag= d (210..231)
 FT /note= "oligonucleotide 1"
 FT exon 211..253
 FT /*tag= a
 FT intron 254..355
 FT /*tag= b
 FT exon 356..1715
 FT /*tag= c
 FT primer_bind complement(845..865)
 FT /*tag= f
 FT /note= "oligonucleotide 3"
 FT primer_bind 1109..1129
 FT /*tag= e
 FT /note= "oligonucleotide 2"
 FT primer_bind 1867..1890
 FT /*tag= g

FT XX EP779037-AL. /note= "oligonucleotide 4"

PN XX

PD XX 18-JUN-1997.

PF XX 27-SEP-1990; 96EP-00202943.

PR XX 27-SEP-1989; 89EP-00202436.

PR XX 17-AUG-1990; 90EP-00202231.

PR XX 27-SEP-1990; 90EP-00202565.

XX (KONN) GIST-BROCADES NV.

PA (STAM) DSM NV.

PI Van Paridon PA, Veenstra AE, Luiten RGM, Selten GCM;

PI Van Gorcom RFM, Van Hartingsveldt W;

DR WPI; 1997-312513/29.

DR P-PSDB; AAW15124.

XX Fungal phytase - releases inorganic phosphate from myoinositol phosphate,

PT useful to prepare animal feed and reduce phytate levels in manure.

XX Example 8; Fig 6; 6ipp; English.

PS Genomic DNA (AAT65137) comprises the phytase gene locus of *Aspergillus*

CC ficum and includes a coding sequence, interrupted by a single intron,

CC for the 467-amino acid enzyme (AAW15124). The DNA sequence was deduced

CC from clones pAF 2-3, pAF 2-6 and pAF 2-7, which were identified in

CC genomic DNA using probes (see also AAT65138-40) based on CNBR peptides

CC (AAW15128-29) of the phytase. PCR primers (AAT65144-47) based on gene

CC sequences were used to amplify a full-length cDNA clone (AAT65136) for

CC the phytase. Characterisation of the phytase gene will allow large-scale

CC prodn. of phytase in transformed host cells for use e.g. in the food and

CC animal feed industries, and for reducing phytate levels in manure.

CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to

CC correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated

CC on 25-MAR-2003 to correct PI field.) (Updated on 17-OCT-2003 to

CC standardise OS field)

XX

SQ Sequence 6756 BP; 1615 A; 1714 C; 1712 G; 1715 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1-96e-233	Length:	6756
Score:	2353.00	Matches:	448
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.79%	Indels:	0
DB:	2	Gaps:	0

US-10-089-364-4 (1-449) x AAT65137 (1-6756)

Qy 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21

Db 369 CTGGCAGTCCCGCGCTCGAGAAATCAATCCAGTTGCGATACGGTCGATCAGGGGTATCAA 428

Qy 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41

Db 429 TGCCTCTCCGAGACTTCGCATCTTTGGGGTCAATACGCACCGCTCTCTCTCTCTCTCTCT 488

Qy 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61

Db 489 GAATCGGTCACTCCCTGAGGTGCCCGCGATGACAGTCACTTTCGTCAGGTCTC 548

Qy 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIle 81

Db 549 TCCCGTCATGAGCGCGGTATCCGACCGACTCCCAAGGGCAAGAAATATCTCGCTCTCATT 608

Qy 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101

Db 609 GAGGAGATCCAGCAGACCGACCCACTTTTGACGGAATAATATGCTTCTCTCTCTCTCTCTCT 668

Qy 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121

Db 669 AACTACACCTTGGGTGGAGATGACCTGACTTCCTTCGGAGAACAGAGCTAGTCACTCC 728

Qy 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141

Db 729 GGCATCAAGTTCTACCGCGGTACGAATCGCTCACAGGAACATCGTTCCATTCTCCGAA 788

Qy 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161

Db 789 TCCCTCTGGCTCCAGCCGCTGATCCCTCCGCAAGAAATTCATCGAGGGTCTCCAGAGC 848

Qy 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181

Db 849 ACCAAGCTTGAGGGATCTCTGTCGCCAGCCCGGCGCATCGTGCCTCAAGATCGAGCTGTC 908

Qy 182 IleSerGluAlaSerSerSerAsnThrLeuAspProGlyThrCysThrValPheGlu 201

Db 909 ATTTCCGAGGCCAGCTCATCCACAACACTCTCGACCCAGGCACCTGCTGCTCTCTCGAA 968

Qy 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221

Db 969 GACAGCGAATTGGCGGATACCGTCGAAGCCAAATTTCACCGCCACGTTCTGCTCCCTCCATT 1028

Qy 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241

Db 1029 CGTCAACGCTTGGAGAGACGACTGTCCGGTGTGACTCTCACAGACACAGAAAGTACCTAC 1089

Qy 242 LeuMetAspMetCysSerPheAspThrIleSerThrValAspThrLysLeuSer 261

Db 1089 CTCATGACATGTGCTCTCTCGACACCATCTCCACCAGCACCGTCGACCAAGCTGTGCC 1148

Qy 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281

Db 1149 CCCTTCTGTGACCTGTTTACCCATGAGAAATGAGATCACTACGACTACTCTCCAGTCTCTG 1208

Qy 282 LysLysTyrTyrGlyHisGlyValaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301

Db 1209 AAAAAGTATTACGGCCATGTTGCGAGGTAAACCCGTCCGCCCGACCCAGGGGGTCTGGTAC 1268

Qy 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321

Db 1269 GCTAACGAGCTCATCGCCGCTCGACCCACTCGCTGTCCACGATGACACCGATTCCCAAC 1328

Qy 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341

Db 1329 CACACTTTTGGACTCGAGCCCGCTACCTTTCCGCTCAACTCTACTCTCTACCGGACTTT 1388

Qy 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361

Db 1389 TCGCATGACAAACGCATCACTCCATTCTCTTTCCTTTAGGTCTGTACACGGCACATAAG 1448

Qy 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381

Db 1449 CCGCTATCTACACGACCGGTGGAGATATACCCAGACAGATGATGATCTGCTGCTGTGG 1508

Qy 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401

Db 1509 ACGGTTCCGTTGCTTCGCGTTGTACGTGAGATGATGATGATGATGATGATGATGATGAT 1568

Qy 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421

Db 1569 CCGTGTGCTGCTTGTGTTATGATGCGGTGTCCCGCTGCATGATGATGATGATGATGATGAT 1628

Qy 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441

Db 1629 GCTTTGGGAGATGTATCCCGGATAGCTTTGTGAGGGGGTTGAGCTTTGTAGATCTGGG 1688

Qy 442 GlyAspTrpAlaGluCysPheAla 449

Db 1689 GGTGATTGGCGGAGTGTGTTTGTCT

RESULT 12

Db 1449 CCCTATCTACACGACCGTGGAGATATACCCACAGACATGATCTCGTCTGCTGG 1508
 QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 Db 1509 ACGTTCCGTTTCTTCGCTTTGTAGTTCAGTGCAGATGATGAGTGTGAGCGGAGGAG 1568
 QY 402 ProLeuValArgValLeuValAenAspArgValProLeuHisGlyCysProValAsp 421
 Db 1569 CCGCTGGTCCGTCTCTGTTAATGATCGCTGTCCCGCTGCATGGGTCCGCTTGAT 1628
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 1629 GCTTTGGGAGATGATACCCCGGATAGCTTTGTGAGGGGTGTGAGCTTTGCTAGATCTGG 1688
 QY 442 GlyAspTirAlaGluCysPheAla 449
 Db 1689 GGTGATGGCGGAGTGTGTGCT 1712
 RESULT 13
 ABN85592
 ID ABN85592 standard; DNA; 1344 BP.
 XX
 AC ABN85592;
 XX
 DT 17-SEP-2002 (first entry)
 XX
 DE Aspergillus niger phyA related polynucleotide 5.
 XX
 KW Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; gene; ds.
 XX
 OS Aspergillus niger.
 XX
 XN CN1333363-A.
 XX
 PD 30-JAN-2002.
 XX
 PF 12-JUL-2000; 2000CN-00117245.
 XX
 PR 12-JUL-2000; 2000CN-00117245.
 XX
 PA (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.
 XX
 PI Chen Z, Yang L, Fang L;
 XX
 DR WPI; 2002-305615/35.
 XX
 PT Phytase gene sequence and application in yeast thereof.
 XX
 PS Disclosure; Fig 5; 48pp; Chinese.
 XX
 CC The invention relates to a coded phytase gene sequence suitable for
 CC secretion and expression in yeast and its application. It is mainly
 CC characterised by removing nucleotide sequence of +45--1146 bit from phyA
 CC total length structure gene sequence, removing Aspergillus niger signal
 CC peptide coded sequence of +1-44 and +147-+159, connecting a part of
 CC signal peptide code sequence suitable for secretion and expression at 5'
 CC end and connecting a restriction endonuclease site at 3' end. The
 CC different carriers can be connected into said gene sequence so as to form
 CC a recombinant plasmid with different functions and after the recombinant
 CC plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia
 CC yeast, finally the invented Pasteur Pichia yeast engineering bacterium
 CC (CCTCC NO:M200005) can be obtained through the screening process. By
 CC using the invention the industrial process of phytase bio-expression can
 CC be successfully implemented. The present sequence is that of a
 CC polynucleotide of the invention
 XX
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 Alignment Scores:
 Pred. No.: 3, 73e-234 Length: 1344
 Score: 2350.00 Matches: 447
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.78% Mismatches: 0

Query Match: 99.66% Indels: 0
 DB: 6 Gaps: 0
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 Db 1 CTGGCAGTCCAGCCCTCTAGAAATCAATCTCTTGTGATACCTGATCAGGGTTTACAA 60
 QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 Db 61 TGTTCCTCCGAGACTTCTCATCTTTGGGTCAATACGCACCATTTCTTCTCTCTGGCAAC 120
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 121 GAATCTGTCTATCTCCCTCAGGTGCCCGCATGTAGAGTCACTTTCGCTCAGCTCCTT 180
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
 Db 181 TCCAGACATGGAGCTAGATATCCACCGACTCCAGGGTAAGAAATACCTCCGCTCTTATT 240
 QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 241 GAGGAGATCCAGCAGAACGCTACCACTTTGACGGAAATATGCTTCTCTGAAGACATAC 300
 QY 102 AsnTyrSerLeuGlyAlaAspSerLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
 Db 301 AACTACTCTTTGGGTGCAGATGACCTGACTCCATTCCGGAGAACAGAGCTTGTCACTCC 360
 QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 361 GGTATCAAGTTCTACAGAGATACGAATCTTTGACAAGAAACATGTTCCATTCATCAGA 420
 QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 421 TCCTCTGTTCTCTAGAGTTATCGCTCCGGTAAGAAATTCATCGAGGTTTCCAGAGC 480
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 Db 481 ACTAAGCTGAAGGATCCCTAGAGCCAGCCAGGTCAATCTCTCCAAAGATCCAGCTTGT 540
 QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 Db 541 ATTTCCGAGGCTCTTCTATCCACACACTCTTGACCCAGGTACTTGTACTGTCTTCGAA 600
 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 Db 601 GACTCTGAATTGGCCGATACTGTGAGGCCAATTTCACTGCCACTTTCGTCCCATCCATT 660
 QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 Db 661 AGACAAAGACTGGAGAGACGACTGTCCGGTGTACTCTTACTGACACTGAAGTTACTTAC 720
 QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
 Db 721 CTTAAGACATGTGTCTCTTCGACACTATCTCCACTTACCGTCGACACCAAGCTGTCC 780
 QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 781 CCATTCTGTGACCTGTTTCAACCATGACGATGGATCAACTACGACTACTTTCAGTCCCTTG 840
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 841 AAAAAGTATTACGGTTCATGGTGCAGGTAACCCATTGGGTCCCAACCCAGGGTGTGGTTAC 900
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 901 GCTAACGAGTTGATCGCCAGACTGACCCACTCTCTCTCCACGATGACACTCTTCCAAC 960
 QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 Db 961 CACACTTTGGACTCTTCTCCAGCTTACCTTTCCATTGAACCTACTATTGTGACGTGACTTT 1020

QY 202 AspSerGluLeuAlaaspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db |||||
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QY 222 ArgGlnArgGluAlaAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db |||||
1502 CGTCAACGTCGTGAGAACGACCTGTCGGGTGTGACTCTCACAGACACAGAGTGACCTAC 1561
QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db |||||
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QY 262 ProPheCysAspLeuPheThrHisAspGluTyrIleAsnTyrAspTyrLeuGlnSerLeu 281
Db |||||
1622 CCCTTCGTGACCTGTTCACCCATGAGATGATCACTACGACTACCTCCAGTCTCTTG 1681
QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db |||||
1682 AAAAAGTATTACGGCCATGGTGCAGGTAAACCGCTCGGCCGACCCAGGGCGTCCGGCTAC 1741
QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
Db |||||
1742 GCTAACGAGCTCATCCGCCCTCTGACCCACTCGCTCTGCCATGACACCACTTCCAA 1801
QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db |||||
1802 CACACTTTGGACTCGAGCCCGGCTACTTTCCGCTCACTCTACTCTCTACGGGACTTT 1861
QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db |||||
1862 TCGCATGACACACGGCATCTCCATCTCTTTGCTTTAGGTCTGTACAAACGGCCTAAG 1921
QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
Db |||||
1922 CCGCTATCTACACGACCGCTGGAGATATACCCAGACAGATGGATTCTCGTCTGCTGG 1981
QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
Db |||||
1982 ACGTTCCGTTTGTCTTCGCGTTTGTACCTCGAGATGATGATGTCAGGCGGAGCAGGAG 2041
QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db |||||
2042 CCGCTGTCGCTGCTTGGTTAATGATCGCGTTGTCCCGCTGCATGGGTGTCCGGTTGAT 2101
QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db |||||
2102 GCTTTGGGGAGATGTACCCGGGATAGCTTTGTGAGGGGGTGTAGCTTTGTAGATCTGGG 2161
QY 442 GlyAspTrpAlaGluCysPheAla 449
Db |||||
2162 GGTGATTGGCGGAGTGTGTTTGCT 2185

Search completed: October 24, 2004, 13:39:01
Job time : 862 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 15:51:50 ; Search time 806 Seconds
(without alignments)
2854.393 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

Sequence: 1 MUAVPASRNQSCDVTVDQY.....SFVRLGFARSGGDWAECFA 449

Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delopt 6.0, Delext 7.0

Searched: 3407233 seqs, 2561960514 residues

Total number of hits satisfying chosen parameters: 6814466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2353	99.8	1404	15	US-10-079-709-33 Sequence 33, Appl
2	2353	99.8	2665	17	US-10-662-914-1 Sequence 1, Appli
3	2353	99.8	6756	15	US-10-079-709-31 Sequence 31, Appl
4	2350	99.7	2665	17	US-10-662-914-21 Sequence 21, Appl
5	2350	99.7	2665	17	US-10-662-914-27 Sequence 27, Appl
6	2349	99.6	2665	17	US-10-662-914-7 Sequence 7, Appli
7	2349	99.6	2665	17	US-10-662-914-17 Sequence 17, Appl
8	2349	99.6	2665	17	US-10-662-914-19 Sequence 19, Appl
9	2349	99.6	2665	17	US-10-662-914-23 Sequence 23, Appl
10	2349	99.6	2665	17	US-10-662-914-33 Sequence 33, Appl
11	2347	99.5	2665	17	US-10-662-914-5 Sequence 5, Appli
12	2347	99.5	2665	17	US-10-662-914-15 Sequence 15, Appl
13	2347	99.5	2665	17	US-10-662-914-29 Sequence 29, Appl
14	2347	99.5	2665	17	US-10-662-914-31 Sequence 31, Appl
15	2346	99.5	2665	17	US-10-662-914-11 Sequence 11, Appl
16	2346	99.5	2665	17	US-10-662-914-25 Sequence 25, Appl
17	2346	99.5	2665	17	US-10-662-914-39 Sequence 39, Appl
18	2345	99.4	2665	17	US-10-662-914-35 Sequence 35, Appl
19	2345	99.4	2665	17	US-10-662-914-41 Sequence 41, Appl
20	2343	99.4	2665	17	US-10-662-914-37 Sequence 37, Appl
21	2343	99.4	2665	17	US-10-662-914-68 Sequence 68, Appl
22	2342	99.3	2665	17	US-10-662-914-43 Sequence 43, Appl
23	2341	99.3	2665	17	US-10-662-914-49 Sequence 49, Appl
24	2341	99.3	2665	17	US-10-662-914-51 Sequence 51, Appl
25	2340	99.2	2665	17	US-10-662-914-53 Sequence 53, Appl
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27	2339	99.2	2665	17	US-10-662-914-47 Sequence 47, Appl
28	2327	98.7	2665	17	US-10-662-914-55 Sequence 55, Appl
29	2327	98.6	1515	9	US-09-929-060-5 Sequence 5, Appli
30	2255	95.6	1332	9	US-09-929-060-4 Sequence 4, Appli
31	1829	81.8	1426	15	US-10-442-538-168 Sequence 168, App
32	1833	77.7	1404	15	US-10-442-538-162 Sequence 162, App
33	1826	77.2	1426	15	US-10-442-538-140 Sequence 140, App
34	1818	77.1	1426	15	US-10-421-112-3 Sequence 3, Appli
35	1818	77.1	1426	15	US-10-442-538-117 Sequence 117, App
36	1806	76.6	1404	15	US-10-442-538-164 Sequence 164, App
37	1618.5	68.6	1455	17	US-10-662-914-9 Sequence 9, Appli
38	1617.5	68.6	1425	14	US-10-213-990-23 Sequence 23, Appl
39	1617.5	68.6	1455	14	US-10-213-990-22 Sequence 22, Appl
40	1617.5	68.6	1455	17	US-10-662-914-3 Sequence 3, Appli
41	1617.5	68.6	1571	14	US-10-062-948-10 Sequence 10, Appl
42	1617.5	68.6	1571	17	US-10-776-104-10 Sequence 10, Appl
43	1610.5	68.3	1398	10	US-09-803-454-19 Sequence 19, Appl
44	1610.5	68.3	1404	15	US-10-442-538-166 Sequence 166, App
45	1534	65.1	1443	15	US-10-369-493-36558 Sequence 36558, A

ALIGNMENTS

RESULT 1
US-10-079-709-33
; Sequence 33, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/079,709
 FILING DATE: 02-FEB-2002
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/233,510
 FILING DATE: 20-JAN-1999
 APPLICATION NUMBER: 07/688,578
 FILING DATE: 24-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Murashige, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 24615-20026.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-327-7250
 TELEFAX: 415-327-2951
 INFORMATION FOR SEQ ID NO: 33:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1404 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Aspergillus ficum* (*Aspergillus niger*)
 STRAIN: NRRL 3135
 US-10-079-709-33

Alignment Scores:
 Pred. No.: 1,57e-272 Length: 1404
 Score: 2353.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 99.79% Indels: 0
 DB: 15 Gaps: 0

US-10-089-364-4 (1-449) x US-10-079-709-33 (1-1404)

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 162 ThrLysLeuLysAspProAlaGlnProGlyGlnSerSerProLysIleAspVal 181
 538 ACCAAGCTGAAGGATCCTCGTCCAGCCCGGCAATCGTCCGCCAAGATCGACGTGGTC 597
 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
 598 ATTTCGAGGCGAGCTCATCCAAACACTCTCGACCCAGGACCTGCACTGCTTCGAA 657
 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 658 GACAGCGAATTGGCCGATACCGTTCGAAGCCAAATTCACGCCACGTTGCTCCCTCCATT 717
 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 718 CGTCAACGCTGGAGAACGACCTGTCGGGTGACTCTCACACACACAGAAAGTGACCTAC 777
 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
 778 CTCATGACATGTGCTCTTCGACACATCTCCACGACACCGTCGACACCAAGCTGCTC 837
 262 ProPheCysAspLeuPheThrHisAspGluThrIleAsnTyrAspTyrLeuGlnSerLeu 281
 838 CCCTTCTGTGACCTGTTCAACCATGACGAATGGATCAACTACGACTACCTCCAGTCTTG 897
 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 898 AAAAAGTATTACGGCCATGGTTCAGGTAAACCCGCTCGGCCGACCCAGGGCGCTGCTAC 957
 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 958 GCTAACGAGCTCATCGCCCGCTGACCCACTCGCCTGTCCACGATGACACACAGTTCCAAC 1017
 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 1018 CACACTTTGGACTCGAGCCGGGTACCTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1077
 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 1078 TCGCATGACAAACGCGATCATCTCCATTCTTTGCTTAGTCTGTGTACAACGGCAGCTAAG 1137
 362 ProLeuSerThrThrThrValGluAsnIleThrThrAspGlyPheSerSerAlaTrp 381
 1138 CCGTATCTTACCAGCCGCTGGAGAAATATCACCCAGACAGATGGATTCGTCTGCTTGG 1197
 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
 1198 ACGGTTCGGTTGCTTCGGGTTTGTACGTGAGATGATGACAGTGTCAAGCGGAGAGAG 1257
 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
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 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 1318 GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTGTAGCTTTGTAGATCTGGG 1377
 442 GlyAspTrpAlaGluCysPheAla 449
 1378 GGTGATTGGCGGAGTGTTTTGCT 1401

RESULT 2

US-10-662-914-1
 ; Sequence 1, Application US/10662914
 ; Publication No. US20040126844A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lei, Xingen
 ; APPLICANT: Mullaney, Edward J
 ; APPLICANT: Ullah, Abul H.J.

2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 58 CTGCGAGTCCCGCTCGAGAAATCAATCCAGTTGCGATACGGTCGATCAGGGGTATCAA 117
 22 CysPheSerGluThrSerHisLeuTyrGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 118 TGCCTCTCCGAGACTTCGCATCTTTGGGGTCAATACCGACCGCTTCTTCTCTCGGCAAC 177
 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 178 GAATCGGTCATCTCCCTGAGGTGCCCGCGATGACAGTCACTTCGCTCAGTCTCTC 237
 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
 238 TCCCGTCATGAGCGCGGTATCCGACCGACTCCAAAGGGCAAGAAATATCCCGCTCTCAT 297
 82 GluGluIleGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuThrTyr 101
 298 GAGGAGATCCAGCAGAACCGCACCACTTTTACCGAAATATGCTTCTTGAAGACATAC 357
 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSer 121
 358 AACTACAGCTTGGGTGAGATGACCTGACTCCCTTCGAGACACAGAGCTAGTCACTCC 417
 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 418 GGCATCAAGTTCTACACGCGGTACGAATCGCTCACAAAGGAACATCGTTCCATTTCGGA 477

; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES

; FILE REFERENCE: 19603/4261

; CURRENT APPLICATION NUMBER: US/10/662,914

; PRIOR FILING DATE: 2003-09-15

; PRIOR APPLICATION NUMBER: 60/410,736

; PRIOR FILING DATE: 2002-09-13

; NUMBER OF SEQ ID NOS: 69

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2665

; TYPE: DNA

; ORGANISM: Aspergillus niger

; US-10-662-914-1

Alignment Scores:

Pred. No.:	4,466-272	Length:	2665
Score:	2353.00	Matches:	448
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	99.79%	Indels:	0
DB:	17	Gaps:	0

US-10-089-364-4 (1-449) x US-10-662-914-1 (1-2665)

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QY	22	CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaSer	41
DB	902	TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGCGTCTCTCTCTGGCAAC	961
QY	42	GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu	61
DB	962	GAATCGGTCACTCCCTGAGTGCCCGCGAGTCAGAGTCACATTTGCTCAGTCTCTC	1021
QY	62	SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIle	81
DB	1022	TCCGCTCATGAGCGCGGTATCCGACCGACTCCAAAGGGCAAGAAATACTCCGCTCTCAT	1081
QY	82	GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheIleLysThrTyr	101
DB	1082	GAGGAGATCCAGCAGAACCGCACCACTTTGACGGAAATATGCTTCTCTGAAGACATAC	1141
QY	102	AsnTyrSerLeuGlyValaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer	121
DB	1142	AACATACACTTGGGTGCAGATGACTGCTCCCTTCGAGACAGAGACTAGTCAACTCC	1201
QY	122	GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg	141
DB	1202	GGCATCAAGTCTTACAGCGGTACGAAATCGCTCAAGGAACATCGTTCCATTCATCGGA	1261
QY	142	SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer	161
DB	1262	TCCCTGCTGCTCCAGCGGTGATCCCTCCGCGCAAGAAATTCATCGAGGGCTTCAGAGC	1321
QY	162	ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal	181
DB	1322	ACCAAGCTGAAGGATCCTCGTCCCGAGCCCGCCCAATCGTCCCAAGATCGAGTGGTC	1381
QY	182	IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu	201
DB	1382	ATTTCCGAGGCGAGTCAATCCAAACAACACTCTCGACCCAGGCACCTGCACTGTCTCGAA	1441
QY	202	AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle	221
DB	1442	GACAGCGAATTTGGCGGATACCGTGAAGCCCAATTTACCGCCAGCTTCGTCCTCCCTCAT	1501
QY	222	ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr	241
DB	1502	CGTCAAGCTCGGAGACGACCTGCTCCGGTGTGACTCTCAAGACACAGAAAGTGACCTAC	1561
QY	242	LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer	261

DB	1562	CTCATGGAGCATGTGCTCTCTCGACACCATCTCCACAGACCGTCCGACACCAAGCTGTCC	1621
QY	262	ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu	281
DB	1622	CCCTTCTGTGACCTGTTACCCATGACGAATGGATCAACTAGCACTACCTCCAGTCTCTTG	1681
QY	282	LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr	301
DB	1682	AAAAAGTATTACGGCCATGGTGCAGTAACCCGCTCGGCCCCACACGAGGGCTCGGCTAC	1741
QY	302	AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn	321
DB	1742	GCTAACGAGCTCATCGCCGCTCTGACCCACCTGCTGCCAGATGACACCAATGCCAAC	1801
QY	322	HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe	341
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QY	362	ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr	381
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DB	1982	ACGGTTCGCTTTCGCTTCGCTTGTACGTCGAGATGATGATGTCAGCGCGAGCAGGAG	2041
QY	402	ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValasp	421
DB	2042	CGCTGCTCGCTGCTTCTGTTAATGATCGGTTGTCGCGCTGCATGGGTGTCGGTTGAT	2101
QY	422	AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly	441
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QY	442	GlyAspTrpAlaGluCysPheAla	449
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RESULT 3

US-10-079-709-31

; Sequence 31, Application US/10079709

; Publication No. US20030119163A1

; GENERAL INFORMATION:

; APPLICANT: Robert F.M. Van Gorcom

; APPLICANT: Willem Van Hartingsveldt

; APPLICANT: Petrus A. Van Paridon

; APPLICANT: Annemarie B. Veenstra

; APPLICANT: Rudolf G.M. Luttin

; APPLICANT: Gerardus Seiten

; TITLE OF INVENTION: Cloning and Expression of Microbial

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morrison & Foerster

; STREET: 545 Middlefield Road, Suite 200

; CITY: Menlo Park

; STATE: California

; COUNTRY: USA

; ZIP: 94025-3471

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; SOFTWARE:

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/079,709

; FILING DATE: 02-FEB-2002

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/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/233,510
/ FILING DATE: 20-JAN-1999
/ APPLICATION NUMBER: 07/688,578
/ FILING DATE: 24-MAY-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Murashige, Kate H.
/ REGISTRATION NUMBER: 29,959
/ REFERENCE/DOCKET NUMBER: 24615-20026.00
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-327-7250
/ TELEFAX: 415-327-2951
/ INFORMATION FOR SEQ ID NO: 31:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 6756 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Aspergillus ficuum (Aspergillus niger)
/ STRAIN: NRRL 3135
/ IMMEDIATE SOURCE:
/ LIBRARY: lambda AF
/ CLONE: pAF2-3, pAF2-6, pAF2-7
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/ LOCATION: 210..253
/ FEATURE:
/ NAME/KEY: intron
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/ NAME/KEY: exon
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/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: join(210..253, 356..1715)
/ OTHER INFORMATION: /codon_start= 210
/ OTHER INFORMATION: /product= "Phytase"
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: 210..380
/ FEATURE:
/ NAME/KEY: mat_peptide
/ LOCATION: 381..1712
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/ OTHER INFORMATION: phosphatase"
/ OTHER INFORMATION: /product= "Phytase"
/ OTHER INFORMATION: /evidence= EXPERIMENTAL
/
/ US-10-079-709-31

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Alignment Scores:
Pred. No.: 2,04e-271 Length: 6756
Score: 2353.00 Matches: 448
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.79% Indels: 0
DB: 15 Gaps: 0

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US-10-089-364-4 (1-449) x US-10-079-709-31 (1-6756)

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QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaIle 81
DB 549 TCCCGTCATGAGCGCGGTATCCGACCGACTCCAGGGCAAGAAATACCTCCGCTCTCAT 608
QY 82 GluGluIleGlnAlaSerAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
DB 609 GAGGAGATCCAGCAAGAACCGACCTTTGACGGAATAATATGCTTCTCTGAAGACATAC 668
QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGlnGlnLeuValAsnSer 121
DB 669 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGAGAACAGAGAGTAGTCAACTCC 728
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
DB 729 GGCATCAAGTTCTACCAAGCGGTACGAATCGCTCACAAGGAACATCGTTCATTCATCCGA 788
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
DB 789 TCCTCTGGCTCCAGCCCGCTGATCGCTCGGCAAGAAATTCATCCAGGGCTTCAGAGC 848
QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspVal 181
DB 849 ACCAAGCTGAAGGATCCTCGTGCCAGCGCGCAATCGTCGCCCAAGATCGACGTGGTC 908
QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
DB 909 ATTTCGAGGCGCAGCTCATCCACAACACTCTCGACCCAGGCACCTGCTGCTTCGAA 968
QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
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DB 1029 CGTCAAGCTCTGGAGAACAGACCTGTCGGGTGTGACTCTCACAGACACAGAAGTGACCTAC 1088
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DB 1089 CTCATGGACATGTGCTCTTCGACACCATCTCCACCAGCACCCGTCGACACCAAGCTGTC 1148
QY 262 ProPheCysAspLeuPheThrHisAspGluTyrIleAsnTyrAspTyrLeuGlnSerLeu 281
DB 1149 CCCTTCTGTGACCTGTTCACCCATGACATGGATCACTACGACTACCTCCAGTCTCTTG 1208
QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
DB 1209 AAAAAGTATTACGGCCATGGTGCAGGTAAACCGCTCGGCCGCCACCCAGGGCGTGGCTAC 1268
QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
DB 1269 GCTAACGAGCTCATCGCCCTGTGACCCACTCGCTCTCCAGATGACACAGATTCACAC 1328
QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
DB 1329 CACATTTGGACTCGAGCCCGGTACTCTTCGCTCACTCACTCTCTACGCGGACTTT 1388
QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
DB 1389 TCGCATGACAAACGGCATCATCTCTCTTTGCTTTAGTCTGTGTCAACGGCAGCTAAG 1448
QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
DB 1449 CCGTATCTACCGACCGGTGGAGATATCACCCAGACAGATGGATTCGTCTGCTTGG 1508
QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
DB 1509 ACGGTTCCGTTGCTTCGGTTTGTAAGTACGTGAGATGATGAGTGTGAGCGGAGCAGGAG 1568
QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421

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Db      1569  CCGCTGGTCCGCTGCTTGGTTAATGATCGCTGTCCCGCTGCATGGGTCCGGTTGAT 1628
QY      422  AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db      1629  GCTTTGGGAGAGATGATACCGGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 1688
QY      442  GlyAspTrrAlaGluCysPheAla 449
Db      1689  GGTGATGGCGGAGTGTGTTTGTCT 1712

RESULT 4
US-10-662-914-21
; Sequence 21, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLIUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-21

Alignment Scores:
Pred. No.: 1,036-271 Length: 2665
Score: 2350.00 Matches: 447
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.78% Mismatches: 0
Query Match: 99.66% Indels: 0
DB: 17 Gaps: 0

US-10-089-364-4 (1-449) x US-10-662-914-21 (1-2665)

QY      2  LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
Db      842  CTGGCAGTCCCGCTCGAGAATCAATCCAGTTGGATACGTCGATCAGGGGTATCAA 901
QY      22  CysPheSerGluThrSerHisLeuTrrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
Db      902  TGCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGCTTCTTCTCTGGCMAAC 961
QY      42  GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db      962  GAATCGGTCACTCCCTTCGAGTGCCCGCGGATCGAGTCACTTTCGTCAGGTCTCTC 1021
QY      62  SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIle 81
Db      1022  TCCCGTCATGAGCGCGGTATCCGACCGACTCCAGGGGCAAGAATCTCCGCTCTCAAT 1081
QY      82  GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db      1082  GAGGAGATCCAGCAGACGCGACCACTTTGACGGAAATATGCTTCTCTGAAGACATAC 1141
QY      102  AsnTyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db      1142  AACTACAGCTTGGGTGCGATGACCTGACTCCCTTCGAGAACAGAGAGTAGTCAACTCC 1201
QY      122  GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db      1202  GGATCAGATTCTACAGCGGTACGATCGCTCACAGGAACATCGTTCCATTCATCGGA 1261
QY      142  SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161

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Db      1262  TCCTCTGGCTCCAGCGCGTGTATCGCTCCGGCAAGAAATTCATCGAGGGCTTCAGAGC 1321
QY      162  ThrLysLeuLysAspProArgIadGlnProGlyGlnSerSerProLysIleAspValVal 181
Db      1322  ACCAAGCTGAAGAGATCCTGTGTCAGCCCGCGCAATCGTCGCCCAAGATCGACGTGTC 1381
QY      182  IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
Db      1382  ATTTCCGAGGCCAGCTCATCCCAACACTCTGACCCCGAGGCACTGCTGCTCTCGAA 1441
QY      202  AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db      1442  GACAGCGAATTCGCCGATACCGTCCAAGCCAAATTTACCGCCACGTTGCTCCCTCCATT 1501
QY      222  ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db      1502  CGTCAACGCTCTGGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAACTGACCTAC 1561
QY      242  LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db      1562  CTCATGGACATGTGCTCCTTCGACACCATCTCCACAGCACCGTCGACACCAAGCTGTCC 1621
QY      262  PropheCysAspLeuPheThrHisAspGluTrrpIleAsnTyrAspTyrLeuGlnSerLeu 281
Db      1622  CCCTTCTGTGACCTGTTCACCCATGACGAATGATCAACTACGACTACCTCCAGTCTTGT 1681
QY      282  LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db      1682  AAAAAAGTATTACGGCCATGGTGCAGGTAAACCGCTCGGCCCGACCCAGGGGTCTGGGTAC 1741
QY      302  AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
Db      1742  GCTAACGAGCTCATCGCCGCTCGACCCACTCGCTGTCCAGATGACACAGTTCACAC 1801
QY      322  HisthrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db      1802  CACACTTTGGACTCGAGCCGGCTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTT 1861
QY      342  SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db      1862  TGGCATGACAAAGCGCATCATCTCCATTCTCTTTGTTTGGTCTGTACACGGCACTAAG 1921
QY      362  ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db      1922  CCGCTATCTACACGACCGTGGAGATATACCCAGACAGATGGATTTCTGCTCTCTGG 1981
QY      382  ThrValPropheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
Db      1982  ACGGTTCCGTTTGTCTTCGCTTTGTACGTCGAGATGATGAGTGTTCAGGCGGAGCAGGAG 2041
QY      402  ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db      2042  CCGCTGGTCCCGTGTCTTGGTTAATGATCGCGTGTTCGCGCTGCATGGGTGTCCGGTTGAT 2101
QY      422  AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db      2102  GCTTTGGGAGATGTACCCGGATAGCTTTGTGAGGGGTTGAGCTTTGTAGATCTGGG 2161
QY      442  GlyAspTrrAlaGluCysPheAla 449
Db      2162  GGTGATGGCGGAGTGTGTTTGTCT 2185

RESULT 5
US-10-662-914-27
; Sequence 27, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLIUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914

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; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-27

Alignment Scores:
Pred. No.: 1,03e-271 Length: 2665
Score: 2350.00 Matches: 447
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.78% Mismatches: 0
Query Match: 99.66% Indels: 0
DB: 17 Gaps: 0

US-10-089-364-4 (1-449) x US-10-662-914-27 (1-2665)

Qy 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyThrGln 21
Db 842 CTGGCAGTCCCGCCCTCGAGAAATCAATCAGTTGGATATCGATCAGGTATCAA 901

Qy 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
Db 902 TGCTTCTCCAGAGACTTCGCATCTTTGGGGTCAATACGCACCGTTCTTCTCTGGCAAC 961

Qy 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db 962 GAATCGGTGCATCTCCCTGAGGTGCCCGCGGATCGAGTCACTTTCGTCTAGGTCTC 1021

Qy 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
Db 1022 TCCGTCATGGAGCGCGGTATCCGACCGACTCCCAAGGGCAAGAAATACTCGGCTCTCAT 1081

Qy 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db 1082 GAGGAGATCAGCAGAAACGCGACCACTTTGACGMAAATAATGCTTCTCCCTGAAGACATAC 1141

Qy 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db 1142 AACTACAGCTTGGTGCAGATGACTGACTCCCTTCGAGAACACAGGAGCTAGTCAACTCC 1201

Qy 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db 1202 GGCAATCAAGTTCTACCAAGCGTACGAATCGTCAACAAGGAACATCGTTCATCCGA 1261

Qy 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
Db 1262 TCCCTCTGGCTCCAGCCGCGTATCGCTCCGGCAAGAAATTCATCGAGGGCTTCACAGC 1321

Qy 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db 1322 ACCAAGCTAAGATCTCTGTGCCAGCCCGGCCAAATCGTCGCCCAAGATCGAGTGTC 1381

Qy 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
Db 1382 ATTTCCGAGGCGAGTCAATCAACAACACTCTCGACCCAGGACCTGCACTGTCTTCGAA 1441

Qy 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db 1442 GACAGCGAATTTGGCCGATACCGTCGAAGCCAATTTACCGCCAGCTTCGTCCCCCTCCATT 1501

Qy 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db 1502 CGTCAACGCTCGAAGACGACCTGTCCGCTGTGACTCTCCACAGACACAGAAAGTCACTAC 1561

Qy 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db 1562 CTCATGGGACATGTGCTCTCGACCACTATCCACGACCGCTCGACACCAAGCTGTCC 1621

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Db 842 CTGGAGTCCCGCTCGAGAAATCAATCCAGTTCGATACCGGTGCATCAAGGGTATCAA 901
 QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 Db 902 TGCCTCTCCGAGACTTCGCATCTTTGGGTCAATACGCACCCGTTCTTCTCTCGCAAC 961
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 962 GAATCGGTCACTCCGCTGAGGTGCCCGCGGATGCAGAGTCACATTGCTCAGTCTCTC 1021
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
 Db 1022 TCCCGTCAATGGACCGCGGTATCCGACCGACTCAAGGGCAAGAAATACTCCGCTCTCAT 1081
 QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 1082 GAGGAGATCCAGACAGCGACCACTTTGACGGAATAATATGCTTCTCGAAGACATAC 1141
 QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluValAsnSer 121
 Db 1142 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGGAGTAGTCAACTCC 1201
 QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
 Db 1202 GGCAATCAAGTTCTACCAAGCGGTACGAATCGCTCAAGGAAACATCGTTCCATTCACCGA 1261
 QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
 Db 1262 TCCTCTGCTCCAGCGCGGTATGCCCTCCGGCAAGAAATCATCGAGGCTTCCAGAGC 1321
 QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
 Db 1322 ACCAAGCTGAAGATCCTCGTGCCCGAGCCGCAATCGTCCGCCAAGATCGAGTGTGTC 1381
 QY 182 IleSerGluAlaSerSerSerAsnAsnThrIleAspProGlyThrCysThrValPheGlu 201
 Db 1382 ATTTCCGAGGCGAGCTCATCCAAACAACTCTCGACCCAGGCACTCGACCTGTCTTCGAA 1441
 QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
 Db 1442 GACAGCGAATGGCGATACCGTGAAGCCAAATTTACCGCCAGCTTCGTCCTCCCTCCAT 1501
 QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
 Db 1502 CGTCAAAGTCTGGAGAACGACTGTCGGTGTGACTCTCACAGACACAGAAGTGACCTAC 1561
 QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
 Db 1562 CTCATGGACATGTGCTCTTCGACACCACTCTCCACGACCGTCGACCGCTCGAACAGTGTCC 1621
 QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 1622 CCCTCTGTGACCTGTTCACCATGACAGAAATGATCAACTACGACTACTCCAGTCCCTTG 1681
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 1682 GAAAGATATTACGGCCATGTGTGAGTAACCCGCTCGGCCCGACCCAGGGGTGCGCTAC 1741
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 1742 GCTAACAGAGCTCATCGCCCGCTGTACCCACATCTCCACGATGACACCAAGTTCACAC 1801
 QY 322 HisThrLeuAspSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
 Db 1802 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCAACTCTACTCTCTACCGCGACTTT 1861
 QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
 Db 1862 TCGCATGACACGCAATCATCTCCATCTCTTTGCTTAGTCTGTACACCGCACTTAAG 1921
 QY 362 ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381

Db 1922 CCGCTATCTACCAACGCGTGGAGAAATATCACCCAGACAGATGGATTCTCGTCTGCTTGG 1981
 QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGlnGlu 401
 Db 1982 ACGGTTCGGTTTGCCTTCGCTTGTACGTCGAGATGATGCAGTGTCAAGCGGAGCAGAG 2041
 QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
 Db 2042 CCGCTGGTCCGCTGCTTGTGTTAATGATCGCTGTCCGCTGCATGGGTGTCGGTTGAT 2101
 QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
 Db 2102 GCTTTGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGTAGATCTGG 2161
 QY 442 GlyAspTrpAlaGluCysPheAla 449
 Db 2162 GGTGATGGCGGAGTGTTTTGCT 2185
 RESULT 7
 US-10-662-914-17
 ; Sequence 17, Application US/10662914
 ; Publication No. US20040126844A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lei, Xingen
 ; APPLICANT: Mullaney, Edward J
 ; APPLICANT: Ullah, Abul H.J.
 ; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
 ; FILE REFERENCE: 19603/4261
 ; CURRENT APPLICATION NUMBER: US/10/662,914
 ; CURRENT FILING DATE: 2003-09-15
 ; PRIOR APPLICATION NUMBER: 60/410,736
 ; PRIOR FILING DATE: 2002-09-13
 ; NUMBER OF SEQ ID NOS: 69
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 17
 ; LENGTH: 2665
 ; TYPE: DNA
 ; ORGANISM: Aspergillus niger
 US-10-662-914-17
 Alignment Scores:
 Pred. No.: 1,35e-271 Length: 2665
 Score: 2349.00 Matches: 447
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.78% Mismatches: 0
 Query Match: 99.62% Indels: 0
 DB: 17 Gaps: 0
 US-10-089-364-4 (1-449) x US-10-662-914-17 (1-2665)
 QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
 Db 842 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTCGATACGGTCAAGGGTATCAA 901
 QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
 Db 902 TGCCTCTCCGAGACTTCGCATCTTTGGGTCAATACGCACCGTCTCTCTCTCGCAAC 961
 QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
 Db 962 GAATCGGTCACTCCGCTGAGGTGCCCGCGGATGCAGAGTCACTTTCGCTCAGTCTCTC 1021
 QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
 Db 1022 TCCCGTCAATGGACCGCGGTATCCGACCGACTCCAGGGCAAGAAATACTCCGCTCTCAT 1081
 QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
 Db 1082 GAGGAGATCCAGACAGCGACCACTTTGACGGAATAATATGCTTCTCGAAGACATAC 1141
 QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluValAsnSer 121
 Db 1142 AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGGAGTAGTCAACTCC 1201

122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
1202 GGCATCAAGTTTACCAGCGGTACGAATCGCTACAGGAACATCGTTCCATTCATCCGA 1261
142 SerSerGlySerSerArgValIleAlaSerGlyLysPheIleGluGlyPheGlnSer 161
1262 TCCTCTGGCTCCAGCGCGGTGATCGCTCGGCAAGAAATTCATCAGAGGCTCCAGAGC 1321
162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
1322 ACCAAGCTGAAGATCCTCGTCCAGCGGCAATCGTCCGCCAAGATCGACGTGGTC 1381
182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
1382 ATTTCCGAGGCGAGCTCATCCAAACACTCTCGACCCAGGACCTGCACTGCTTCGAA 1441
202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
1442 GACAGCGAATGGCCGATACCGTCCGAAGCAATTTCAACGCCACGTTCCGCTCCATT 1501
222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrIleuThrAspThrGluValThrTyr 241
1502 CECTCAACGCTCGAGAACACCTGTCGGGTGACTCTCACACACACAGAAAGTGCCTAC 1561
242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
1562 CTCATGGACATGTCCTCTCGACCACTCTCCACGACCACTCCACGACACCGTCCAGCCTGTC 1621
262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
1622 CCCTTCTGTGACCTGTTCCCATGACGAATGATCAACTACGACTACCTCCAGTCTCTG 1681
282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
1682 AAAAAATATTACGGCCATGTGTCAGGTAAACCGCTCGGCCGACCCAGGCGGTGCGCTAC 1741
302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
1742 GCTAACAGAGCTATCGCCCGCTCTGACCCACTCGCCCTGTCCACGATGACACAGTCCAAC 1801
322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
1802 CACACTTTGGACTCGAGCCCGGTACTCTTCGCTCAACTCTACTCTCTACGCGGACTTT 1861
342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
1862 TCGCATGACAAACGSCATCATCTCCATTTCTCTTTGCTTAGGTCTGTACAAACGGCACCTAAG 1921
362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
1922 CCCTATCTACCAACAGCGTGGAGATATACCCACGACAGATGATTCCTCTGCTGTGG 1981
382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
1982 ACGGTTCCGTTTCTTCGCTTGTAGTGTGAGATGATGATGATGATGATGATGATGATGAT 2041
402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
2042 CCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2101
422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
2102 GCCTTGGGAGATGATCCCGGATAGCTTTGTGAGGGGCTTGTGCTTGTAGATCTGGG 2161
442 GlyAspTrpAlaGluCysPheAla 449
2162 GGTGATTGGCGGAGTGTGTTGCT 2185

RESULT 8

US-10-662-914-19

; Sequence 19, Application US/10662914

; Publication No. US20040126844A1

GENERAL INFORMATION:

; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.

; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES

; FILE REFERENCE: 19603/4261

; CURRENT APPLICATION NUMBER: US/10/662,914

; CURRENT FILING DATE: 2003-09-15

; PRIOR APPLICATION NUMBER: 60/410,736

; PRIOR FILING DATE: 2002-09-13

; NUMBER OF SEQ ID NOS: 69

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 19

; LENGTH: 2665

; TYPE: DNA

; ORGANISM: Aspergillus niger

; US-10-662-914-19

Alignment Scores:

Pred. No.: 1,35e-271 Length: 2665
Score: 2349.00 Matches: 447
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.78% Mismatches: 0
Query Match: 99.62% Indels: 0
DB: 17 Gaps: 0

US-10-089-364-4 (1-449) x US-10-662-914-19 (1-2665)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerCysAspThrValAspGlnGlyTyrGln 21
DB 842 CTGGCAGTCCCGCTCGAGAAATCAATCCAGTTGGATACGGTGCATCAGGGGTATCAA 901
QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
DB 902 TGTCTTCCGAGACTTCGATCTTTGGGTCAATAGCACCGTCTCTCTCTGGCAAC 961
QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
DB 962 GAATCGGTCTATCTCCCTGAGGTGCGCGGATGACAGTCACTTTCGCTCAGGTCTC 1021
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIle 81
DB 1022 TCCCGTCATGAGCGGCTATCCGACCGACTCCAGGGCAAGAAATATGCTTCTTCAATT 1081
QY 82 GluGluIleGlnAsnAlaThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
DB 1082 GAGGATCCAGCAGAACCGCACCTTTGACGGAAATATGCTTCTTGAAGACATAC 1141
QY 102 AsnTyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
DB 1142 AACTACAGCTTGGGTGCAGATGACTCCCTTCGGAGAACAGAGCTAGTCAACTCC 1201
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
DB 1202 GGATCAAGTTTACACAGCGGTACGAATCGCTCAGGCAAGAAATTCATCAGGGCTTCCAGAGC 1261
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysPheIleGluGlyPheGlnSer 161
DB 1262 TCCTCTGGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCAGGGCTTCCAGAGC 1321
QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
DB 1322 ACCAAGCTGAAGATCCTCGTCCCGACCGCGCAATCGTCCGCCAAGATCGACGTGGTC 1381
QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
DB 1382 ATTTCCGAGGCGAGCTCATCCAAACACTCTCCACCCAGGACCTGCACTGCTTCGAA 1441
QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
DB 1442 GACAGCGAATGGCCGATACCGTCCGAAGCAATTTCAACGCCACGTTCCGCTCCATT 1501
QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241

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Db      1502 CGTCAACGCTGGAGAACGACCTGTCCGGTGTGACTCTCAACAGACACAGAAAGTGACCTAC 1561
QY      242  LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db      1562 CTCATGGACATGTCCTTCGACCATCTCCACAGACCCGTCGACACCAAGCTGTCC 1621
QY      262  ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
Db      1622 CCCTTCTGTGACCTGTTACCCATGACGAATGATCACTACCACTCTCCAGTCTCTTG 1681
QY      282  LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db      1682 AAAAAGATTATACGGCCATGTGTGAGGTAAACCCGCTCGGCCGACCCAGGGCGTCCGCTAC 1741
QY      302  AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspThrHisAspThrSerAsn 321
Db      1742 GCTAACGAGCTATCCGCGCTGTAGCCCATCTCCCTGTCCAGATGACACCACTTCCAAAC 1801
QY      322  HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db      1802 CACACTTTGGACTCGAGCCGCGGTACTCTTTCCGCTCAACTCTACTCTCTACGGGACTTT 1861
QY      342  SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db      1862 TCGCATGACAAACGGCATCATCTCCATTCTCTTTGCTTTAGTCTGTACAAACGGCACTAAG 1921
QY      362  ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db      1922 CGGCTATCTACACGACCCGCTGGAGAAATATACCCAGACAGATGATCTCGTCTGCTGG 1981
QY      382  ThrValProPheAlaSerArgLeuTyrValGluMetGlnCysGlnAlaGluGlnGlu 401
Db      1982 ACGGTTCCGTTTGTCTCGCGTTTGTACGTCGAGATGATGACAGTGTGACGCGGAGGAG 2041
QY      402  ProLeuValArgValLeuValAsnAspArgValProLeuHisGlyCysProValAsp 421
Db      2042 CCGCTGGTCCGTTCTGTGTTAATGATCGCGTGTCCGCTGCATGGGTGTCGCGTTGAT 2101
QY      422  AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db      2102 GCTTTGGGAGATGTACCCGGGATGACTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 2161
QY      442  GlyAspTrpAlaGluCysPheAla 449
Db      2162 GGTGATTGGCGGAGTGTCTTGTCT 2185

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RESULT 9

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US-10-662-914-23
; Sequence 23, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLIUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-23

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Alignment Scores:

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Pred. No.: 1,35e-271 Length: 2665
Score: 2349.00 Matches: 447
Percent Similarity: 100.00% Conservative: 1

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Best Local Similarity: 99.78% Mismatches: 0
Query Match: 99.62% Indels: 0
DB: 17 Gaps: 0
US-10-089-364-4 (1-449) x US-10-662-914-23 (1-2665)
QY      2  LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
Db      842  CTGGCAGTCCGCCCTCGAGAAATCAATCAGTTGCGATACGGTTCGATCAGGGGTATCAA 901
QY      22  CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
Db      902  TGTCTTCTCCGAGACTTCGCATCTTTGGGGTCAATACGACCGCTTCTTCTCTCTGGGCAAC 961
QY      42  GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db      962  GAATCGGTCTATCTCCCTGAGGTGCCCGCGGATGCGAGTCACTTTGCTCAGGTCCTC 1021
QY      62  SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
Db      1022  TCCGTCATGGAGCGCGGTATCCGACCGACTCCAGGGCAAGAAATACCTCCGCTCTCAT 1081
QY      82  GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db      1082  GAGGAGATCCAGCAGAACCGGACCTTTGACGGAAATATGCTTCTCTGAGACATAC 1141
QY      102  AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db      1142  AACTACAGCTTGGGTGCAGATGACCTGATCCCTTCGGAGAACAGAGCTAGTCAACTCC 1201
QY      122  GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db      1202  GGCATCAAGTTCTACAGCGGTACGAATCGCTCAACAGGAACATCGTTCCATTCATCCA 1261
QY      142  SerSerglySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
Db      1262  TCCTCTGGCTCCAGCGCGGTGATCGCTCCCGCAAGAAATTCATCGAGGCTTCCAGAGC 1321
QY      162  ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db      1322  ACCAAGCTGAAGGATCCCTCGTCCCGACCCGCGCAATCGTCCCGCAAGATCGACGTGTC 1381
QY      182  IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGln 201
Db      1382  ATTTCGAGGCGAGCTCATCCACACACTCTCGACCCAGGACCTGCTGCTGCTCTCTTCCA 1441
QY      202  AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db      1442  GACAGCGAATTGGCGGATACCGTCAAGCCCAATTTACCGCCACGTTGCTGCCCTCCATT 1501
QY      222  ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db      1502  CGTCAACGCTCTGGAGAACGACCTGTCCGGTGTGACTCTCACAGACACAGAAAGTGACCTAC 1561
QY      242  LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db      1562  CTATGACATGTGCTCTTCGACACCATCTCCACCGACCGTCCAGGCGGCGGCGTGGCTTCC 1621
QY      262  ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
Db      1622  CCCCTTCTGTGACCTGTTTCAACCATGACGAATGGATCAACTACGACTACTCTCCAGTCTTG 1681
QY      282  LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db      1682  AAAAAGATTATACGGCCATGTGTGAGGTAAACCCGCTCGGCCGACCCAGGGCGTGGCTTAC 1741
QY      302  AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspThrHisAspThrSerAsn 321
Db      1742  GCTAACGAGCTCATCGCGCGTGTGACCATCTCCGCTGTCCAGATGACACCACTTCCAAAC 1801
QY      322  HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db      1802  CACACTTTGGACTCGAGCCGCGGTACTCTTTCCGCTCAACTCTACTCTCTCTACGGGACTTT 1861

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Db      2162 GGTGATTGGCGGAGTGTCTTGGCT 2185
RESULT 11
US-10-662-914-5
; Sequence 5, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; PRIOR FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-5
Alignment Scores:
Pred. No.:      2,366-271      Length:      2665
Score:          2347.00      Matches:      447
Percent Similarity: 99.78%      Conservative: 0
Best Local Similarity: 99.78%      Mismatches: 1
Query Match:      99.53%      Indels:      0
DB:              17          Gaps:        0
US-10-089-364-4 (1-449) x US-10-662-914-5 (1-2665)
QY      2  LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
Db      842  CTGGGAGTCCCGCGCTCGAGAAATCAATCCAGTTGCGATACGATCAGGGGTATCAA 901
QY      22  CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPheSerLeuAlaAsn 41
Db      902  TGCTTCTCCAGACTTCGCATCTTTGGGGTCCATACGACCGACCTTCTCTCTCGCAAAAC 961
QY      42  GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db      962  GAATCGGTATCTCCCTGAGTGGCGCGCGATGCGAGTCACTTCGCTCAGGTCTCTC 1021
QY      62  SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIle 81
Db      1022  TCCCGTCAATGGACGCGGTATCCGACCGACTCCAAAGGGCAAGAAATACTCCGCTCTCATT 1081
QY      82  GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db      1082  GAGGAGATCCAGCAGAACGCGACCACTTTGACGGAATAATATGCTTCTCTGAAGACATAC 1141
QY      102  AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db      1142  AACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAACAGAGCTAGTCACTCC 1201
QY      122  GlyIleLysPheTyrGluArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db      1202  GGCATCAAGTTCTTACACGCGGTACGAATCGCTTCAAGGAACATCGTTCATTATCCGA 1261
QY      142  SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
Db      1262  TCCTCTGCTCCAGCGGTGATCCCTCCCGCAAGAAATCATCGAGGGCTTCAGAGC 1321
QY      162  ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db      1322  ACCAAGCTGAAGATCCTCGTCCCGAGCCCGGCAATCGTCCCAAGATGACGTGGTC 1381
QY      182  IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201

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Db      1382  ATTTCCGAGCGCAGCTCATCCAAACAACACTCTCGACCCAGGCACCTGCATGCTCTTCGAA 1441
QY      202  AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db      1442  GACAGCGAATTGGCCGATACCGTTCGAAGCAATTTTCCCGCCACAGTTCGTCCTCCCTCAT 1501
QY      222  ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db      1502  CGTCAACGCTCGGAGAACACCTGTCGGGTGACTCTTCACAGACACAGAAGTGACCTAC 1561
QY      242  LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db      1562  CTATGAGCATGTGCTCTTCGACACCATCTCCACGACACCGTCGACACCAAGCTGTCC 1621
QY      262  ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrIleuGlnSerLeu 281
Db      1622  CCCTTCTGTGACTGTTCACCCATGACGAATGATCACTACGACTACCTCCAGTCCCTTG 1681
QY      282  LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db      1682  AAAAGTATTACGGCATGTGCGAGTAACCCGCTCGGCCCGACCCAGGGCGTTCGGCTAC 1741
QY      302  AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
Db      1742  GCTAACGAGCTCATCGCCGTCTGACCCACTCGCTGTCCACGATGACACCAAGTCCCAAC 1801
QY      322  HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrIleuTyrAlaAspPhe 341
Db      1802  CACACTTTGGACTCGAGCCCGGTACTCTTCGCTCAACTCTACTCTCTACCGGACTTT 1861
QY      342  SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db      1862  TGCATGACACAGGCATCATCTCCATTCTCTTTGTTAGTCTGTACACGGCACTAAG 1921
QY      362  ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db      1922  CGCTATCTACCAACGACCGTGGAGAAATATCACCCAGACAGATGGATTCTCGTCTCTTGG 1981
QY      382  ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGlnGlu 401
Db      1982  ACGSTTCGGTTCGCTTCGCTTGTACGTCGAGATGATGATGATGATGATGATGATGATGAT 2041
QY      402  ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db      2042  CGCTGGTTCGGTTCGCTTGTAAATGATCGGTGTCGCTGATGATGATGATGATGATGATGAT 2101
QY      422  AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db      2102  GCTTGGGGAGATGTACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGGG 2161
QY      442  GlyAspTrpAlaGluCysPheAla 449
Db      2162  GGTGATTGGCGGAGTGTCTTGGCT 2185
RESULT 12
US-10-662-914-15
; Sequence 15, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 15
; LENGTH: 2665
; TYPE: DNA

```


ORGANISM: Aspergillus niger
US-10-662-914-15

Alignment Scores: 2.36e-271 Length: 2665
Pred. No.: 2347.00 Matches: 447
Score: 2347.00
Percent Similarity: 99.78% Conservatives: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.53% Indels: 0
DB: 17 Gaps: 0

US-10-089-364-4 (1-449) x US-10-662-914-15 (1-2665)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
DB 842 CTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTGCGATACGGTGCATCGAGGGTATCAA 901
QY 22 CysPheSerGluThrSerHisLeuTyrGlnTyrAlaProPhePheSerLeuAlaAsn 41
DB 902 TGGCTTCCGAGACTTCGCACTTTTGGGTCAATAGCACCGTTCCTCTCTGGCAAC 961
QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
DB 962 GAATCGGTCACTCCCTCGAGTGGCGCGCGGATCGAGACTCACTTCGCTCAGGTCCTC 1021
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
DB 1022 TCCCGTCATGAGCGCGGTATCCGACCGACTCCCGGGCAAGAAATCACTCCGCTCTCAT 1081
QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
DB 1082 GAGGAGATCCAGCAGACGCGACCACTTTGAGGAAATATGCTTCCTCGAAGACATAC 1141
QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
DB 1142 AACTACAGCTGGGTGCGAGATGACCTGACTCCCTTCGGAGAACAGAGCTAGTCAACTCC 1201
QY 122 GlyTyrLeysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
DB 1202 GGATCAAGTCTACCAAGCGGTAGCAATCGCTCAAGGAAACATCGTTCATTCATCGA 1261
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
DB 1262 TCCTCTGGCTCCAGCCGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCAGAGC 1321
QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
DB 1322 ACCAAGCTGAAGGATCCTCGTCCCGCAGCCCGCCCAATCGTCCCAAGATCGACGTGGTC 1381
QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGlu 201
DB 1382 ATTTCCGAGGCCAGCTCATCCACACACTCTCCAGCCAGCACCTGCACTGTCTTCGAA 1441
QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
DB 1442 GACAGCGAAATGGCCGATACCGTGAAGCAATTTCAACCGCACGTTTCGCTCCCTCCATT 1501
QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
DB 1502 CGTCAACGCTCGGAGAACGACCTGTCCGGTGTGACTCTCAACAGACACAGAGTGACCTTAC 1561
QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrThrValAspThrLysLeuSer 261
DB 1562 CTCATGGACATGTGCTCTTCGACACCACTTCACACAGCCAGCACCGTCGACCAAGCTGCC 1621
QY 262 ProPheCysAspLeuPheThrHisAspGluTyrIleAsnTyrAspTyrLeuGlnSerLeu 281
DB 1622 CCGTCTCTGTGACCTGTTCAACCATGACGAAATGATCAACTACGATACCTCCAGTCCCTTG 1681
QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
DB 1682 AAAAAGTATTACGGCATGGTGCAGGTAAACCGCTCGGCCCGACCCAGGGGTGCGCTAC 1741

QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
DB 1742 GCTAACGAGCTCATCGCCGCTGTGACCCACTCGCCTGTCCAGATGACACCGAGTCCAAC 1801
QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
DB 1802 CACACTTTGGACTCGAGCCCGGCTACCTTTCCGCTCACTCTACTCTCTACCGGGACTTT 1861
QY 342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
DB 1862 TCGCATGACACCGCATCACTCCATCTCTTTGCTTTAGTCTGTACAAACGGCACTAAG 1921
QY 362 ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyr 381
DB 1922 CCGCTATCTACACGACCGTGGAGAAATATCACCCAGACAGATGGATTCGCTCTGCTGG 1981
QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
DB 1982 ACGGTTCCGTTTTCCTTCGCGGTTTGTACGTCAGATGATGCAGTGTCCAGCGGAGCAGAG 2041
QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
DB 2042 CCCTGGTCCGTCCTTGGTTAATGATCGGTTTCCCGCTGCATGGGTCTCCGGTTGAT 2101
QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
DB 2102 GCTTTGGGAGATGATCCCGGATAGCTTTGTGAGGGGTGAGCTTTGTCTAGATCTGGG 2161
QY 442 GlyAspThrAlaGluCysPheAla 449
DB 2162 GGTGATTTGGCGGAGTGTTTTGTCT 2185

RESULT 13

US-10-662-914-29
; Sequence 29, Application US/10662914
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Kingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-29

Alignment Scores: 2.36e-271 Length: 2665
Pred. No.: 2347.00 Matches: 447
Score: 2347.00
Percent Similarity: 99.78% Conservatives: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.53% Indels: 0
DB: 17 Gaps: 0

US-10-089-364-4 (1-449) x US-10-662-914-29 (1-2665)

QY 2 LeuAlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGln 21
DB 842 CTGGCAGTCCCGCCCTCGAGAAATCAATCCAGTTGCGATACGGTGCATCGAGGGTATCAA 901
QY 22 CysPheSerGluThrSerHisLeuTyrGlnTyrAlaProPhePheSerLeuAlaAsn 41
DB 902 TGGTCTCCGAGACTTCGCACTTTTGGGTCAATAGCACCGCTTCCTCTCTGGCAAC 961
QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61

Db 962 GAATCGGTATCTCCCTGAGTGTCCCGCGGATGAGAGTCACTTTCCGCTCAGGTCCCT 1021
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIle 81
Db 1022 TCCCGTCAATGAGCGGGGTATCCAGCGATCCCAAGGGCAAGAAATATCCGCTCTCAAT 1081
QY 82 GluGluIleGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db 1082 GAGGAGATCCAGCAGAACGCGACCACTTTGACGGAAATATGCTTCTCTGAAGACATAC 1141
QY 102 AsnTyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnLeuValAsnSer 121
Db 1142 AACTACAGTTGGTGCAGATGACCTGACTCCCTTCGGAGAACAGAGGCTAGTCAACTCC 1201
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db 1202 GGCATCAAGTTCTACAGCGGTACGATCGCTCACAGGAACATCTGCTCAATTCATCCGA 1261
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysPheIleGluGlyPheGlnSer 161
Db 1262 TCCTCTGGCTCCAGCGCGGTATCGCTCCGGCAAGAAATTCATCGAGGCTTCCAGAGC 1321
QY 162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db 1322 ACCAAGCTGAAGGATCTCTGTCGCCAGCGCGCAATCTGCGCCCAAGATCGACGTGGTC 1381
QY 182 IleSerGluAlaSerSerSerAsnAsnThrLeuAspProGlyTyrCysThrValPheGlu 201
Db 1382 ATTTCCGAGCCAGCTATCCCAACAACATCTCGACCCAGGACCTGCTGCTCGAA 1441
QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db 1442 GACAGCGAATTGGCCGATACCGCTCGAAGCCAAATTCACCGCCACGTTCTGCTCCCTCAT 1501
QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db 1502 CGTCAACGCTCGAGAACGACCTGTCGGTGTGACTCTCACAGACACAGAGTGCCTAC 1561
QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db 1562 CTATCGGACATGTGCTCTTCGACACCACTCTCCACAGACCGCTGACCAAGCTGTCTC 1621
QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
Db 1622 CCCTTCTGTACCTGTTCACCATGACGAATGATCACTACGACTCTCCAGTCCCTTG 1681
QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db 1682 ACAAAGTATTACGGGCATGGTGCAGGTAAACCGCTCGGCCGACCGCGCTCGGTAC 1741
QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerAsn 321
Db 1742 GCTAACGAGCTCATCGCCGCTGACCACTCGCTGTCCAGATGACAGATGTCCAAAC 1801
QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db 1802 CACACTTTGGACTCGAGCGCGGCTACCTTTCGCTCACTCTACTCTCTACGCGGACTTT 1861
QY 342 SerHisAspAsnGlyIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db 1862 TCGCATGACAAGCGGATCATCTCCATCTCTTTGCTTTAGGTCTGTACACGGCACTTAAG 1921
QY 362 ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db 1922 CCGTATCTACCGAGCGGTGAGAAATATCACCCAGACAGATGGATCTCGTCTGCTTGG 1981
QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetGlnCysGlnAlaGluGlnGlu 401
Db 1982 ACGGTTCCGTTGCTTTCGGTTGTACGTCAGATGATGCCAGACAGATGGATCTCGTCTG 2041
QY 402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421

Db 2042 CCCTCGGTCCGTGCTCTTGTGTTAATGATCGCGTGTGCCGCTGCATGGGTCCGGTTGAT 2101
QY 422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
Db 2102 GCCTTCCGGGAGATGTATACCCGGGATAGCTTTGTGAGGGGTTGAGCTTTGCTAGATCTGG 2161
QY 442 GlyAspTrpAlaGluCysPheAla 449
Db 2162 GGTGATTGGCGGAGTGTGTTGCT 2185
RESULT 14
US-10-662-914-31
; Sequence 31, Application US/1066291.4
; Publication No. US20040126844A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xingen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abul H.J.
; FILE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-31
Alignment Scores:
Pred. No.: 2,366-271 Length: 2665
Score: 2347.00 Matches: 447
Percent Similarity: 99.76% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.53% Indels: 0
DB: 17 Gaps: 0
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QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
Db 902 TGCTTCTCCGAGACTTCGCACTTTTGGGTCATACGACCGCTTCTTCTCTCTGSCAAC 961
QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db 962 GAATCGGTCACTCCCTGAGTGCCTGCGCCGATGACAGTCACTTTCGCTCAGTCTCCT 1021
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysTyrSerAlaLeuIle 81
Db 1022 TCCCGTCAATGAGCGGGGTATCCGACCGACTCCAGGGCAAGAAATATCCGCTCTCAAT 1081
QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db 1082 GAGGAGATCCAGCAGAACGCGACCACTTTGACGGAAATATGCTTCTCTGAAGACATAC 1141
QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db 1142 AACTACAGTTGGTGCAGATGACCTGACTCCCTTCGGAGAACAGAGGCTAGTCAACTCC 1201
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db 1202 GGCATCAAGTTCTACAGCGGTACGATCGCTCAAGGAACATCGTTCATTCATCCGA 1261
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
Db 1262 TCCTCTGGCTCCAGCGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGCTTCCAGAGC 1321

162 ThrLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
1322 ACCAAGCTGAAGGATCTCTGGCCCGCGGCAATCGTCGCCCAAGATCGACGGTGC 1381
182 IleSerGluAlaSerSerAsnThrLeuAspProGlyThrCysThrValPheGlu 201
1382 ATTTCGAGGCCAGCTCATCCACACACTCTCGACCCAGCACCTGCACCTGCTTCGAA 1441
202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
1442 GACAGCGAATTGGCCGATACCGTCGAGCAATTCACCGCCACGTTCTGTCCTCCATT 1501
222 ArgGluArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
1502 CGTCAACGCTGGAGACGACCTGTCGGGTGTGACTCTCACAGACAGAAAGTGACCTAC 1561
242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
1562 CTCATGGACATGTGCTCTTCGACACCATCTCCACCCAGCACCGTCGACACCAAGCTGCC 1621
262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
1622 CCCTTCTGTACCTGTTCACCCATGACGAATGGATCAACTACGACTACCTCCAGTCCCTG 1681
282 LysIleTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
1682 GATAAGTATTACGCCCAATGTGAGGTAACCGCTCGGCCCGACCCAGGGCGTCGGCTAC 1741
302 AlaAsnGluLeuLeuAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
1742 GCTAACGAGTCTACGCCGCTCTGACCCACTCGCCTCTCCACGATGACACCAAGTCCAAC 1801
322 HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
1802 CACACTTGGACTCGAGCGGGTACCTTTCGGCTCAACTCTACTCTCTACGGCGACTTT 1861
342 SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
1862 TCGCATGACACGAGCATCATCTCAATCTCTTTCCTTTAGTCTGTACACGGGACCTAAG 1921
362 ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
1922 CCGTATCTACACGACCGTGGAGAAATATCACCCAGACAGATGATTCGTCTGCTGG 1981
382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
1982 ACGGTTCCGTTGCTTCGGCTTTCTAGCTCGAGATGATGCAAGTGTCAAGCGGAGAGAG 2041
402 ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
2042 CCGTGTGTCGGTGTCTGGTTAATGATCGCGTGTTCGGCTGCAATGGGTGTCCGGTTGAT 2101
422 AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
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442 GlyAspTrpAlaGluCysPheAla 449
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RESULT 15
US-10-662-914-11
; Sequence 11, Application US/10662914
; Publication No. US2004012684A1
; GENERAL INFORMATION:
; APPLICANT: Lei, Xinggen
; APPLICANT: Mullaney, Edward J
; APPLICANT: Ullah, Abdul H.J.
; TITLE OF INVENTION: USING MUTATIONS TO IMPROVE ASPERGILLIUS PHYTASES
; FILE REFERENCE: 19603/4261
; CURRENT APPLICATION NUMBER: US/10/662,914
; CURRENT FILING DATE: 2003-09-15

; PRIOR APPLICATION NUMBER: 60/410,736
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 2665
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-662-914-11
Alignment Scores: Length: 2665
Pred. No.: 3,11e-271 Matches: 447
Score: 2346.00
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 1
Query Match: 99.49% Indels: 0
D: 17 Gaps: 0

US-10-089-364-4 (1-449) x US-10-662-914-11 (1-2665)
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Db 842 CTGGCAGTCCCGCTCGAAGATCAATCCAGTTGGATACGATCAGGGGTATCAA 901
QY 22 CysPheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsn 41
Db 902 TGCTTCTCCGAGACTTCGATCTTTGGGTCTATACGACCGCTCTCTCTGGCAAC 961
QY 42 GluSerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeu 61
Db 962 GAATCGGTCTATCTCCCTGAGGTGCGCGCGATGCGAGATCACTTTCGCTCAGGTCTC 1021
QY 62 SerArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIle 81
Db 1022 TCCGTCATCGAGCGCGGTATCCGACGACTCCCAAGGGCAAGAAATACTCCGCTCTCAT 1081
QY 82 GluGluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyr 101
Db 1082 GAGGAGATCCAGACAGACGCGACACCTTTGAGGAAATATGCTTCTTGAAGACATAC 1141
QY 102 AsnTyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSer 121
Db 1142 AACTACAGCTTGGGTGCGAGATGACCTGACTCCCTTCGAGAACAGAGAGTAGTCACTCC 1201
QY 122 GlyIleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArg 141
Db 1202 GGCATCAAGTTCTACACGCGGTACGAATCGCTCAAGGAACATCGTTCATTCATCCGA 1261
QY 142 SerSerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSer 161
Db 1262 TCCCTCTGGCTCCAGCGGTGATCGCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGC 1321
QY 162 ThrIleLysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValVal 181
Db 1322 ACCAAGCTGAAGATCTCTGTCGCCCGCGGCAATCGTCCCGCAAGATCGACGTGGTC 1381
QY 182 IleSerGluAlaSerSerSerAsnThrLeuAspProGlyThrCysThrValPheGlu 201
Db 1382 ATTTCCGAGCGCAGCTCATCCACACACTCTCCAGCCAGCACCTGTCACCTGTCTTCGAA 1441
QY 202 AspSerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIle 221
Db 1442 GACAGCAATTTGGCCGATACCGTGAAGCCCAATTTACCGCCAGCTTCTGCTCCCTCCATT 1501
QY 222 ArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyr 241
Db 1502 CGTCAACGCTCTGGAGAACGACTGTGCGGTGTGACTCTCACAGACAGAAAGTGACCTAC 1561
QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
Db 1562 CTCATGGACATGTGCTCTCTCGACACCATCTCCACCGACCGTCCGACCAAGGTGTCC 1621
QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281

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Db      1622  |||||TCTGTGACCTGTACCCATGACGAATGGATCACTACGACTACCTCCAGTCCCTTG 1681
QY      282   LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
Db      1682  AAAAGATATTAGGCCCATCGTCAGAGTAACCCGCTCGGCCCGGACCCAGGCGTCGGCTAC 1741
QY      302   AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
Db      1742  GCTAACGAGCTCATGCCCGCTGTGACCCACTCGCCTGTCCACGATGACACCACTTCCAAC 1801
QY      322   HisThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPhe 341
Db      1802  CACACTTTGAGACTCGAGCGCGCTACTTTCCGCTCACTCTACTCTCTACGCGACTTT 1861
QY      342   SerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db      1862  TCGCATGACACGGCATCATCTCCATTCTTTGCTTTAGGTCTGTACACGGCACTAAG 1921
QY      362   ProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db      1922  CCGCTATCTTACCACGACCGTGGAGAATATCACCCAGACAGATGGATTCTCGTCTGCTTGG 1981
QY      382   ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
Db      1982  ACGGTTCCGTTTGTCTCGCGTTTGTACGTCGAGATGATGACGTGTCAGCGCGGAGCAGGAG 2041
QY      402   ProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAsp 421
Db      2042  CCGCTGGTCCCGTCTTGTGTTAATGATCGCGTGTCCCGCTGCATGGGGTCCGGTTGAT 2101
QY      422   AlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGly 441
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QY      442   GlyAspTyrAlaGluCysPheAla 449
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Search completed: October 24, 2004, 19:28:59
Job time : 844 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 24, 2004, 13:06:14 ; Search time 5508 Seconds
(without alignments)
2970.486 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

Sequence: 1 MIAVFAIRNQSCDVTDDQY.....SFVRLSFARSGGDWAECFA 449

Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=BST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCCALIGN=200 -THRM SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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-NO.MWAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_est2:.*
3: gb_hic:.*
4: gb_est3:.*
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9: gb_gsl2:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	774.5	32.8	810	7	C0011644 EST799979
C 3	721.5	30.6	880	7	C0004996 EST793331
C 4	689.5	29.2	868	6	CD459861 Fg09_07a1
C 5	634.5	26.9	737	7	C0011643 EST799978
C 6	606	25.7	700	7	CK569249 HO12K16w
C 7	575	24.4	802	8	AQ324539 mgxb0019C
8	547	23.2	603	1	AU248054 AU248054
9	510	21.6	620	6	CD031252 mgmt005xE

C 10	450.5	19.1	586	6	CD030240
C 11	440	18.7	650	5	BQ142672
C 12	414	17.6	544	7	CF862369
C 13	387	16.4	581	1	AJ274007
C 14	387	16.4	1059	7	CN808226
C 15	374.5	15.9	837	8	AQ255459
C 16	368	15.6	526	6	CD056577
C 17	358	15.2	395	7	CN250089
C 18	326	13.8	510	4	BM866254
C 19	323.5	13.7	753	8	AQ163004
C 20	308	13.1	520	6	CD646039
C 21	302.5	12.8	669	8	AQ361495
C 22	296	12.6	275	5	BQ491147
C 23	296	12.6	1019	9	CNS070QI
C 24	290	12.3	405	7	CN249954
C 25	288	12.2	691	6	CA747583
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C 27	277.5	11.8	724	7	CF390509
C 28	273.5	11.6	1019	9	CNS06G8E
C 29	267.5	11.3	978	9	CNS06N99
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C 32	260	11.0	963	9	CNS073L9
C 33	254	10.8	918	7	CF820741
C 34	253	10.7	810	8	AQ161556
C 35	245	10.4	787	9	CNS072VN
C 36	245	10.4	1110	9	CNS06PO9
C 37	244	10.3	922	9	CNS075LP
C 38	241	10.2	914	9	CNS075JG
C 39	240	10.2	746	6	CD645596
C 40	239	10.1	630	1	AJ273121
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ALIGNMENTS

RESULT 1
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LOCUS EST793332 934 bp mRNA linear EST 09-JUN-2004
DEFINITION kb Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
VERSION C0004997
KEYWORDS EST.
SOURCE C0004997.1 GI:48511886
ORGANISM Coccidioides posadasii
Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE
AUTHORS Gardner, M.J. and Cole, G.T.
TITLE Analysis of gene expression in Coccidioides posadasii mycelia and spherules via expressed sequence tags
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST793331
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
Seq primer: M13 Reverse.
Location/Qualifiers
1..934
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Location/Qualifiers
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/strain="C735"
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/clone="CIEAM59"
/dev_stage="spherules"

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/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii spherule cDNA library,
0.4 to 2.3 kb"
/note="Vector: pExpress 1; Site 1: Not 1; Site 2: Eco RV;
Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb"

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ORIGIN

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Alignment Scores:
Pred. No.: 9,41e-84 Length: 934
Score: 811.00 Matches: 150
Percent Similarity: 66.02% Conservative: 54
Best Local Similarity: 48.54% Mismatches: 105
Query Match: 34.39% Indels: 0
DB: 7 Gaps: 0

US-10-089-364-4 (1-449) x C0004997 (1-934)
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Db 4 AGACGAGATCTTGAATGCACTAGTGTCAAGCTCGATACAGTGCACACGACCGTTTGCT 63
QY 28 HisLeuTyrGlyGlnTyrAlaProPhePheSerLeuAlaAsnGluSerValIleSerPro 47
Db 64 CAGCTCTGGGGCCAAATATTCCTCTCTGAAATCAAAAGTCTCCCATCTCTCCG 123
QY 48 GluValProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyAlaArg 67
Db 124 GATGATACCGTCTGGATGCACTATTAATCTTTGCCAAGTCTGTCCCGGCATGGAGCAAG 183
QY 68 TyrProThrAspSerLysGlyLysTyrSerAlaLeuIleGlnGlnAsn 87
Db 184 TATCCACGAGAAAGAAACCGAGCTCTAGCAAACTCTTGATCGATCAAGAAACC 243
QY 88 AlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsnTyrSerLeuGlyAla 107
Db 244 AGCAAGTCTTATGAGGACGACTTCAAGTCTCTGAAAAAATCTTGATGATACGCTGAAGC 303
QY 108 AspAspLeuThrProPheGlyGluGlnGluValAsnSerGlyIleLysPheTyrGln 127
Db 304 GATGATATGACAGAAATTCGGGACACCACTTCAATCTTGGGGCAAAATCTACGAT 363
QY 128 ArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSerSerGlySerArg 147
Db 364 CGTATAGGGTTTGGCGAAGAGATACGACCTGCTGAGTGGCGGGTCTCCGAGG 423
QY 148 ValIleAlaSerGlyLysLysPheIleGluGlnSerThrLysLeuLysAspPro 167
Db 424 GTGATCAAGTCAGCAGAGAGATTTATTCAGGATTCAGAGATCTTGGGCTTGTATCT 483
QY 168 ArgAlaGlnProGlyGlnSerSerProLysIleAspValValIleSerGluAlaSer 187
Db 484 GATGGTTCGAGAGAGATAGACCCCTATGCTCAACTGATTTATCCCTGAGGAGAGTCG 543
QY 188 SerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAspSerGluLeuAlaAsp 207
Db 544 AGTAAACATACCTTGACCATCTTATCGGAAACCTTCGACAGGATTAATTCAGGAAA 603
QY 208 ThrValGluAlaAsnPheThrAlaThrPheValProSerIleArgGlnArgLeuGluAsn 227
Db 604 GAGAGCAGAGAAAAATTCGTGACCTATTTGCGCCCTCCAAATCTTTGACGCGTGTGAAA 663
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QY 248 PheAspThrIleSerThrThrValAspThrLysLeuSerProPheCysAspLeuPhe 267
Db 724 TTCCACACCGTATGTTGACGCGCCGACGAGCAAACTATCTCCATCTTGCAACTCTTC 783
QY 268 ThrHisAspGluTyrIleAsnTyrAspTyrLeuGlnSerLeuLysLysTyrTyrGlyHis 287
Db 784 ACCCCAGGCGAATGGGTTGACTATGACTACTACCAAGTCTCTTGGGAAATATATACAGAT 843

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QY 288 GlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAlaAsnGluLeuIleAla 307
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QY 308 ArgLeuThrHisSerProValHisasp 316
Db 904 CGTCTCAAAACACCCCGCTCAATGAC 930

RESULT 2
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LOCUS EST799979 Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
DEFINITION kb Coccidioides posadasii cDNA clone CIEB041 5' end, mRNA sequence.
ACCESSION C0011644
VERSION C0011644.1 GI:48518533
KEYWORDS EST
SOURCE Coccidioides posadasii
ORGANISM Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE 1 (bases 1 to 810)
AUTHORS Gardner,M.J. and Cole,G.T.
TITLE Analysis of gene expression in Coccidioides posadasii mycelia and
JOURNAL spherules via expressed sequence tags
COMMENT Unpublished (2003)
Other ESTs: EST799978
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
Seq primer: M13 Reverse.

FEATURES
source
1..810
/organism="Coccidioides posadasii"
/mol_type="mRNA"
/strain="C735"
/db_xref="taxon:199306"
/clone="CIEB041"
/dev_stage="spherules"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii spherule cDNA library,
0.4 to 2.3 kb"
/note="Vector: pExpress 1; Site 1: Not 1; Site 2: Eco RV;
Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb"

ORIGIN
Alignment Scores:
Pred. No.: 1.43e-79 Length: 810
Score: 774.50 Matches: 145
Percent Similarity: 69.52% Conservative: 42
Best Local Similarity: 53.90% Mismatches: 79
Query Match: 32.85% Indels: 3
DB: 7 Gaps: 1

US-10-089-364-4 (1-449) x C0011644 (1-810)
QY 176 ProLysIleAspValValIleSerGluAlaSerSerSerAsnAsnThrLeuAspProgly 195
Db 3 CCTATCGTCACTTGTATTCCTCCCTGAAGAGAGTCAATACATACATACACTTGACACTCT 62
QY 196 ThrCysThrValPheGluAspSerGluLeuAlaAspThrValGluAlaAsnPheThrAla 215
Db 63 TTAATCGGAAACTTCGACAGGATTAATTCAGGAAAGAGAGAGAGAGAGAGAGAGAG 122
QY 216 ThrPheValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThr 235
Db 123 CTATTTGGCCCTCCAAATTCCTGAGCGTGTGAAACTCATCTCCCTGGCGCAATATTACG 182
QY 236 AspThrGluValThrTyrLeuMetAspMetCysSerPheAspThrIleSerThrSerThr 255

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183 GTACAGATGTGATACCTCATGATATGCTCTCCACACCGTGATGTGACGCC 242
256 ValAspThrLysLeuSerProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyr 275
243 GAGCGAGANACTATCTCATCTCCCAACTCTTCCACCCAGGCGATGGGTGACTAT 302
276 AspTyrLeuGlnSerLeuLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyPro 295
303 GACTACTACAGTCTCTGGGAATATTACAGATATGGCCAGGACCGCTCGGTCT 362
296 ThrGlnGlyValGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHis 315
363 GAGCAAGGATGGATGATCCACCAAGCACTCATAGCCGCTCTCACAAACACCCCGTCAAT 422
316 AspAspThrSerSerAsnHisThrLeuAspSerProAlaThrPheProLeuAsnSer 335
423 GACTCGACTTCCACCAACCGCACTCTTACCTCTCACCACCGACCTTCCCGTTAAACGCC 482
336 ThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGly 355
483 ACTCTCTACGAGACTTACGCATGATAACACTATGATAACGATCTTACGCGCTTGGGG 542
356 LeuTyrAsnGlyThrLysProLeuSerThrThrValGluAsnIleThrGlnThrAsp 375
543 CTGTTCAATAGACGAGCACTCCCTCTGACCGCATCCGACCCCGCTAGAGTCGGAC 602
376 GlyPheSerSerAlaTrpThrValProPheAlaSerArgLeuTyrValGluMetGln 395
603 GGATTTCTGCTGCGAGGCTCCGTTTGGCGTAGGGCTTACGTTGAGAAGATGAAG 662
396 CysGln-----AlaGluGlnProLeuValArgValLeuValAsnAspArgVal 412
663 TGTGACTGTGTCGCCAAGGAGGATGACGAGTTGTGAGAACTTCTGCTAAATGATCGTT 722
413 ValProLeuHisGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPheVal 432
723 TATCCGCTCCATGGGTGTAACTGAGTACTATTAGGCGCGTGGCGAGTTAATGATTTGTT 782
433 ArgGlyLeuSerPheAlaArgSerGly 441
783 AAGGGGCTGAGCTATGACGCGGCGGG 809

```

```

RESULT 3
CO004996/c
LOCUS
DEFINITION
EST793331 Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb Coccidioides posadasii cDNA clone CIEAM59 3' end, mRNA sequence.
ACCESSION
CO004996
VERSION
CO004996.1 GI:48511885
SOURCE
Coccidioides posadasii
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.

```

```

REFERENCE
1 (bases 1 to 880)
Gardner,M.J. and Cole,G.T.
Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
Unpublished (2003)
Other ESTs: EST793332
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.
Location/Qualifiers
1 .880
/organism="Coccidioides posadasii"
/mol_type="mRNA"
/strain="C735"
/db_xref="taxon:199306"

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JOURNAL

COMMENT

FEATURES

source

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1 .880
/organism="Coccidioides posadasii"
/mol_type="mRNA"
/strain="C735"
/db_xref="taxon:199306"

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/clone="CIEAM59"
/dev_stage="spherules"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii spherule cDNA library,
0.4 to 2.3 kb"
/note="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV;
Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb"

```

ORIGIN

```

Alignment Scores:
Pred. No.: 2,67e-73 Length: 880
Score: 721.50 Matches: 132
Percent Similarity: 73.80% Conservative: 37
Best Local Similarity: 57.64% Mismatches: 57
Query Match: 30.60% Indels: 3
DB: 7 Gaps: 1

US-10-089-364-4 (1-449) x CO004996 (1-880)
QY 223 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 242
Db 880 GAGCGTGTGAAACACTCATCTCCCTGGCGCAATATTACGGTCACAGATGTGATCTACCTC 821
QY 243 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 262
Db 820 ATGGATATGTGCTCTCTTCCACACCGTGATGTGACGCCGCGAGCAAACTATCTCCA 761
QY 263 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 282
Db 760 TTCTCCCAACTCTTCCACCCAGCGAATGGGTGACTATGACTACTACCACTCTCTTGGG 701
QY 283 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 302
Db 700 AAATATTACAGATATGGCGGACGAGCCGCTCGGTGTGAGCAAGGATGGGATTCACC 641
QY 303 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 322
Db 640 AAGNACTCATAGCCCGTCTCATAAACACCCCGTCAATGACTCGACTTCCACCAACCGC 581
QY 323 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 342
Db 580 ACTCTTACTCTTCCACCGACCACTTCCCGCTAAACGCCACTCTCTACGAGACTTCAGC 521
QY 343 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 362
Db 520 CATGATAACACTATGATAAAGCATCTTACGCGCTTGGGCTGTTCATATAGCACGGAACA 461
QY 363 LeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 382
Db 460 CTCCCGCTTGACCGATCCGACCCCGTAGAGTCGGACGAGATTCTTGCCTCGTGGACG 401
QY 383 ValProPheAlaSerArgLeuTyrValGluMetGlnCysGln-----AlaGlu 399
Db 400 GTCCCGCTTGGCGGTAGGGCTTACGTTGAGAAGATGAAGTGTGACTGTCGCCAAGGAAG 341
QY 400 GlnGluProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysPro 419
Db 340 GATGACGAGTTTGTGAGAACTCTTCTAAATGATCGTGTATTATCCGCTCCATGGGTGAAC 281
QY 420 ValAspAlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArg 439
Db 280 GTGGACTCATTTAGCCCGGTGCGAGTTAATGATTTTGTAAAGGGGCTGAGCTATGCAGCG 221
QY 440 SerGlyGlyAspTrpAlaGluCysPhe 448
Db 220 AGCGGGGGAATGTGGACAGATGCTTT 194

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RESULT 4
CD459861/c
LOCUS
DEFINITION
FG09_07a12_A FG09 AAFPC ECORC Fusarium graminearum simple_substrate
Gibberella zeae cDNA clone FG09_07a12, mRNA sequence.

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CD459861
FG09_07a12_A FG09 AAFPC ECORC Fusarium graminearum simple_substrate
Gibberella zeae cDNA clone FG09_07a12, mRNA sequence.

```

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ACCESSION      CD459861
VERSION        CD459861.2
KEYWORDS       GI:486898933
SOURCE         Gibberella zeae
ORGANISM       Gibberella zeae
REFERENCE      1 (bases 1 to 868)
AUTHORS        Watson,R.J., Heys,R., Couroux,P., De Moors,A., Harris,L.J.,
                Hattori,J., Lacroix,C., Masotti,M., Ouellet,T., Robert,L.S.,
                Singh,J.A., Sprott,D. and Tinker,N.A.
TITLE          A cDNA library prepared from Fusarium graminearum grown on a simple
                substrate
JOURNAL        Unpublished (2003)
COMMENT        On Jun 3, 2003 this sequence version replaced gi:31374601.
                Contact: Watson, Robert.J.
                Eastern Cereal and Oilseed Research Centre
                Agriculture and Agri-food Canada
                Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
                CANADA
                Tel: (613) 759-1655
                Fax: (613) 759-1701
                Email: watsonrj@agr.gc.ca.
FEATURES       Location/Qualifiers
                1..868
                /organism="Gibberella zeae"
                /mol_type="mRNA"
                /strain="DAOM 180378"
                /db_xref="taxon:5518"
                /clone="Fg09_07a12"
                /tissue_type="mycelium"
                /dev_stage="Asexual"
                /lab_host="E. coli DH10B"
                /clone_lib="Fg09 AAPC_ECORC_Fusarium graminearum_simple_su
                bstrate"
                /note="Vector: pBluescript II+; Site 1: EcoRI; Site 2:
                XhoI; Fusarium graminearum grown on a simple substrate--
                minimal media supplemented with amino acids."
ORIGIN
Alignment Scores:
Pred. No.:      1,48e-69      Length:      868
Score:          689,50      Matches:    141
Percent Similarity: 64.86%      Conservative: 38
Best Local Similarity: 51.09%      Mismatches: 86
Query Match:     29.24%      Indels:    11
DB:              6          Gaps:       6

US-10-089-364-4 (1-449) x CD459861 (1-868)
Qy 180 valvalleserGluAlaSerSerAsnAsnThrLeuAspProGlyThrCysThrVal 199
Db 842 CTGTGATTCGGAAGAGTCGGGATCAACAACACCATGTCGATGATGATGATGATG 783
Qy 200 PheGlu--AspSerGluLeuAlaAspThr---ValGluAlaAsnPheThrAlaThrPhe 217
Db 782 TTTGAGAGGACGACGACCTGGCGATAACCAACCAACCGCTTGGGGAATAAGTTT 723
Qy 218 ValProSerIleArgGlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThr 237
Db 722 CTGCCTCCCATTCGAGACAGACTCAACAGAGATTGAAAAGGCGCAAGTTGTCGTGAAG 663
Qy 238 GluValThrIleuMetAspMetCysSerPheAspThrIleSerThr-----SerThr 255
Db 662 GAAACTGCTATCTCATGATGATCTGTCCTTCAACACCGTCACACCCCGATGGCGCA 603
Qy 256 ValAspThrIleuSerProPheCysAspLeuPheThrHisAspGluTrpIleAsnTrp 275
Db 602 GTGCAGTCCAG-----TTTGGACCTCTTTCTACAGAAGATTGCGGAAGCTAC 552
Qy 276 AspTyrLeuGlnSerLeuIleLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyPro 295
Db 551 AACTACTGGCAGACTCTCAGCAAGTACTACAAGTACGCGCAACGGTAATGATGGGACCA 492

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Qy 296 ThrGlnGlyValGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHis 315
Db 491 ACACAGGGTGTGGATATGTTAATGAATCATCTCCGGCTGACACGAAGCCGTCAG 432
Qy 316 AspAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPheProLeuAsnSer 335
Db 431 GATGACAACTACGAACACGACATTGGATTCCACCCGAGACGTCCTCCCTCGCAGG 372
Qy 336 ThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGly 355
Db 371 GCTCTGTATGCTGATTTTATGACCAACGACATGCTTCCATCTTTCCGCTATGGGC 312
Qy 356 LeuTyrAsnGlyThrIleProLeuSerThrThrValGluAsnIleThrGlnThrAsp 375
Db 311 CTGTACAACTACACAGGCAAGTTGCGAAACACCACTGTGCCAGCCGTCGGGGCGCAC 252
Qy 376 GlyPheSerSerAlaTrpThrValProPheAlaSerArgLeuTyrValGluMetMetGln 395
Db 251 GGCTACTCATCTGCGTGGTGGTCCCTTTTGGGGCGCGCATGTACGTCGAGAAGCTCGAG 192
Qy 396 CysGlnAla-----GluGln-----GluProLeuValArgValLeuValAsnAspArg 411
Db 191 TCGCGCGCCACCAAGAACAGAGGCGGAGGATGTGAGGGTGTGTGTCATGACCGA 132
Qy 412 ValValProLeuHisGlyCysProValAspAlaLeuGlyArgCysThrArgAspSerPhe 431
Db 131 GTGATGGAGCTTGATACCTGTGGAGGAGATGAGTATGCGNMGTTGCACTCTGGAAGACTTT 72
Qy 432 ValArgGlyLeuSerPheAlaArgSerGlyGlyAspTyrAlaGluCys 447
Db 71 GTAGAGAGCTTGTGCTTTGCTAGAGGAGGACACTGGGATCGATGC 24

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RESULT 5
COO11643/c 737 bp mRNA linear EST 09-JUN-2004
LOCUS EST799978 Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
DEFINITION kb Coccidioides posadasii cDNA clone CIEB041 3' end, mRNA sequence.
ACCESSION COO11643
VERSION COO11643.1 GI:48518632
KEYWORDS EST.
SOURCE Coccidioides posadasii
ORGANISM Coccidioides posadasii
REFERENCE 1 (bases 1 to 737)
AUTHORS Gardner,M.J. and Cole,G.T.
TITLE Analysis of gene expression in Coccidioides posadasii mycelia and
        spherules via expressed sequence tags
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST799979
        Contact: Gardner MJ
        The Institute for Genomic Research
        9712 Medical Center Drive, Rockville, MD 20850, USA
        Tel: 301 838 3519
        Fax: 301 838 0208
        Email: gardner@tigr.org.
FEATURES Location/Qualifiers
        1..737
        /organism="Coccidioides posadasii"
        /mol_type="mRNA"
        /strain="C735"
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        /clone="CIEB041"
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        Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
        kb"
ORIGIN

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Alignment Scores:

Pred. No.: 3,21e-63 Length: 737
 Score: 634.50 Matches: 115
 Percent Similarity: 75.39% Conservatives: 29
 Best Local Similarity: 60.21% Mismatches: 44
 Query Match: 26.91% Indels: 3
 DB: 7 Gaps: 1

US-10-089-364-4 (1-449) x CO011643 (1-737)

QY 261 SerProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSer 280
 Db 737 TCTCCATTGCGCACTCTTACCCAGGGAATGGTTGACTATGACTACTACCACTCT 678
 QY 281 LeuLysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGly 300
 Db 677 CTGGGAATATTACAGATATGGCCAGGAGCCCGCTGGTCTGAGCAGGATGGGA 618
 QY 301 TyrAlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSer 320
 Db 617 TTCACCAAGCAATCATAGCCGCTCTCACAAACACCCCGCTCAATGACTCGACTTCCACC 558
 QY 321 AsnHisThrLeuAspSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAsp 340
 Db 557 AACCGCACTTACCTCTCACCGACCACTTCCCGCTAAACGCCACTCTCTACGCAGAC 498
 QY 341 PheSerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThr 360
 Db 497 TTCAGCCATGATAACACTATGATACGATCTTCACGGCCTTGGGCTGTCTAATGACAG 438
 QY 361 LysProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerAla 380
 Db 437 GAACCACTCCCGCTTACCGCATCCGAGACCCCGTAGAGTCGACGGAATTTCTGGTCG 378
 QY 381 TrpThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGln----- 397
 Db 377 TGGACGTGCCGTTTCCCGTAGGGCTTACGTTGAGAGATGAAGTGTGACTGTGCGCA 318
 QY 398 AlaGluGlnGluProLeuValArgValLeuValAsnAspArgValValProLeuHisGly 417
 Db 317 AGGAAGGATGACGAGTTTGTGAGATCTTGCTAAATGATCGTGTATCCCGTCCATGGG 258
 QY 418 CysProValAspAlaLeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPhe 437
 Db 257 TGTACGTGGCATCATATAGCCGCTGCGAGGTAAATGATTTTGTAAAGGGCTGAGCTAT 198
 QY 438 AlaArgSerGlyGlyAspTrpAlaGluCysPhe 448
 Db 197 GCAGCGACGGGGGAATGTGGACAGATGCTTT 165

RESULT 6

CK569249/c

LOCUS

DEFINITION HO12K16w HO Hordeum vulgare cDNA clone HO12K16 3-PRIME, mRNA

SEQUENCE

ACCESSION CK569249

VERSION CK569249.1 GI:40954823

KEYWORDS EST.

SOURCE Hordeum vulgare

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.

1 (bases 1 to 700)

Zierold, U. and Schweizer, P.

Barley ESTs from pathogen-attacked leaf epidermis

Unpublished (2003)

Contact: Patrick Schweizer

REFERENCE

AUTHORS Transcription Analysis, Cytogenetics Department

TITLE Institute of Plant Genetics and Crop Plant Research (IPK)

JOURNAL Corrensstr. 3, D-06466 Gatersleben, Germany

Tel: 0049 (0)39482-5660

Fax: 0049 (0)39482-5595

Email: schweiz@ipk-gatersleben.de
 Insert Length: 700 Std Error: 0.00
 Plate: 12 row: K column: 16
 Seq primer: T7.

FEATURES

source

1..700
 Location/Qualifiers
 /organism="Hordeum vulgare"
 /mol_type="mRNA"
 /cultivar="Ingrid BC mlo-5"
 /db_xref="GABI:903186"
 /db_xref="taxon:4513"
 /clone="HO12K16"
 /tissue_type="leaf epidermis, 6 h and 24 h post
 inoculation with Blumeria graminis"
 /dev_stage="7 d after germination"
 /lab_host="XL10-Gold"
 /clone_lib="HO"
 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
 cDNA); Site 2: XhoI (3'-end of cDNA); Approximately 5 % of
 the clones correspond to cDNA from the fungi B. graminis
 hordei and tritici, respectively. Due to a cloning
 artefact caused by the kit, in most cases the EcoRI site
 is NOT present, as well as the EcoRI adapter used for
 cloning. To excise the insert, restriction sites upstream
 EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
 due to the cloning system used Blue/white selection for
 recombinants is not 100% reliable. Average insert size is
 1.2 kb"

ORIGIN

Alignment Scores:
 Pred. No.: 6,5e-60 Length: 700
 Score: 606.00 Matches: 117
 Percent Similarity: 70.67% Conservatives: 30
 Best Local Similarity: 56.25% Mismatches: 57
 Query Match: 25.76% Indels: 4
 DB: 7 Gaps: 2

US-10-089-364-4 (1-449) x CK569249 (1-700)

QY 242 LeuMetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSer 261
 Db 681 CTCATGGACCTTTGTCCTTTTGATACAAATGCCAACGAA-----CAAGGTGAAGTCTCT 628
 QY 262 ProPheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeu 281
 Db 627 CCATTCTGCCATTTATTCACTGCTTCTGAATGGCAGCGCTACGACTACTATGAACCGTT 568
 QY 282 LysLysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyr 301
 Db 567 GGAAGTACTACGGCTATTCATGGGTAATCCCTGGAGCCACTCAGGGCGTCGGTTT 508
 QY 302 AlaAsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsn 321
 Db 507 ACTAATGAGCTGATTGACGAGCTCCTCGCTCTCTCTCATCGATCACACAGACCAAT 448
 QY 322 HisThrLeuAspSerSerProAlaThrPheProLeuAsn-----SerThrLeuTyrAla 339
 Db 447 AACACACTTGATCATGACCAAAAGACATTTCTCTCGATAATCAAACTACTCTCTATGCC 388
 QY 340 AspPheSerHisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGly 359
 Db 387 GATTTTACGACGACCAACGACCTCCTAGTATATATGGCTGTGTGTCTCTCTACAAAGAT 328
 QY 360 ThrLysProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSer 379
 Db 327 TCTCCGCCACTCTCAAGACGACGCGTCCAAATCTTCAACGGCTTACGACTATCCACT 268
 QY 380 AlaTrpThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGlu 399
 Db 267 AGCGTACTCTGCTACCGTTTGGTGGCGGTATCTATTTCGAAAGTTGAAATGCCAAGATATA 208
 QY 400 GlnGluProLeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysPro 419

Db	207	GGGAGATTTATCAGGTAATTCGATGATCGGTTCTTCGCTCGAATCTTCGGGC	148
Qy	420	ValAspAlaLeuGlyArgCysThrArgAspSerPheValArgLeuSerPheAlaArg	439
Db	147	GGAGATGAACCTGGGTAGGTACGCTAGATAAATTTGTGATAGCCTGAAATTTGGCGCA	88
Qy	440	SerGlyGlyAspTrpAlaGluCys	447
Db	87	CACGATGAAGATGGTCTGAGTGT	64
RESULT 7			
LOCUS	AQ324539/c		
DEFINITION	mgxb0019C01r CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0019C01r, genomic survey sequence.		
ACCESSION	AQ324539		
VERSION	AQ324539.1	GI:4116391	
KEYWORDS	GSS.		
SOURCE	Magnaporthe grisea (anamorph: Pyricularia grisea)		
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. 1 (bases 1 to 802)		
REFERENCE	Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R., Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.		
AUTHORS	A BAC End Sequencing Framework to Sequence the Magnaporthe grisea Genome		
TITLE	Unpublished (1998)		
JOURNAL	Contact: Dean RA		
COMMENT	Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson University, Clemson, SC 29634 Tel: 864 656 5737 Fax: 864 656 4293 Email: rdean@clemson.edu Seq primer: GGAACAGCTATGACCATG Class: BAC ends High quality sequence stop: 408. Location/Qualifiers 1. 802 /organism="Magnaporthe grisea" /mol_type="genomic DNA" /strain="70-15" /db_xref="taxon:148305" /clone="mgxb0019C01r" /tissue_type="Protoplasts" /lab_host="E. coli DH10B" /clone_lib="CUGI Rice Blast BAC Library" /note="Vector: pBACWICH; Site 1: HindIII; Site 2: HindIII; Rice blast is one of the most devastating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."		
FEATURES	source		
ORIGIN	Alignment Scores: Pred. No.: 3.47e-56 Length: 802 Score: 575.00 Matches: 110 Percent Similarity: 66.50% Conservative: 27 Best Local Similarity: 53.40% Mismatches: 65 Query Match: 24.39% Indels: 4 Dg: 8 Gaps: 2		
US-10-089-364-4 (1-449) x AQ324539 (1-802)			
Qy	229	LeuSerGlyValThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPhe	248

Db	619	CTTAGAGGGTGAACCTCACGCCAAGCGGTGCAGATCATGAGCTTTCGCCGTT	560
Qy	249	AspThrIleSerThrThrValAspThrLysLeuSerProPheCysAspLeuPheThr	268
Db	559	GAGACCGTGGCAGATCCN-----CAAGCCACCTGTTCGAGTTCTGCACGCTGTTTACG	506
Qy	269	HisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLysTyrTyrGlyHisGly	288
Db	505	CAACGAGACTGGGAGGCATATGATATCTCCAGACACTGGGGAAGTGTATGGTTACGC	446
Qy	289	AlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAlaAsnGluLeuAlaArg	308
Db	445	AATGGCAACCCCTGGGCTCCAGCAAGGGTGGCTTCGTCAACGAGCTCATCGGAGG	386
Qy	309	LeuThrHisSerProValHisAspThrSerSerAsnHisThrLeuAspSerSerPro	328
Db	385	CTGCTCCAAAGCCCGTTGAAGACACACAAATACCACTCGAGCTCGACAGGCCCA	326
Qy	329	AlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIle	348
Db	325	TCGACGTTCCACTAGACAAAAGCTGTACGCCGACTTTAGCCATGATACGATATCTG	266
Qy	349	SerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrThrVal	368
Db	265	GGCATCTACGCCCGCTGGGGATTACACGCCACGCCGCCCGCCGATCGGTCCCCAAAG	206
Qy	369	Glu-----AsnIleThrGlnThrAspGlyPheSerSerAlaThrThrValProPhe	386
Db	205	GAGAGAGGAGCGCGCAGGAGCTCAGCGGTTCTCGTCCAGCTGGCGGTACCGTTCCGA	146
Qy	387	SerArgLeuTyrValGluMetGlnCysGlnAlaGluGlnGluProLeuValArgVal	406
Db	145	GCGAGGATGTTTGTGTGAAAAATGACTTGGCGCAGGCGCAACAGGAGGCTTGTGAGAATC	86
Qy	407	LeuValAsnAspArgValValProLeuHisGlyCysProValAlaLeuGlyArgCys	426
Db	85	CTGCTCAACGACAGGGTGACGCCGCTCGAGACTGCGATGCCGACATGGTGGTCTGTC	26
Qy	427	ThrArgAspSerPheVal	432
Db	25	ACGTGAGCAAGTTCGTT	8
RESULT 8			
LOCUS	AU248054		
DEFINITION	AU248054 HL (Lolium multiflorum) Lolium multiflorum cDNA clone HL003501-5, mRNA sequence.		
ACCESSION	AU248054		
VERSION	AU248054.1	GI:46505323	
KEYWORDS	EST.		
SOURCE	Lolium multiflorum (Italian ryegrass)		
ORGANISM	Lolium multiflorum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Poace; Lolium. 1 (bases 1 to 603) Ikeda, S. Lolium multiflorum EST Project Unpublished (2004) Contact: Seishi Ikeda Japan Grassland Farming Forage Seed Association (JFSA) Forage Crop Research Institute (FCRI) Higashiakada 388-5, Nishinasuno, Tochigi 329-2742, Japan Tel: 81-287-37-6755 Fax: 81-287-37-6757 Email: siked67@ffsassoc.or.jp contact: Tadashi Takamizo (takamizo@affrc.go.jp) National Institute of Livestock and Grassland Science, Nishinasuno Resistance gene analog. Location/Qualifiers 1. 603 /organism="Lolium multiflorum"		

/mol_type="mRNA"
/db_xref="taxon:4521"
/clone="HL003E01-5"
/tissue_type="Heat shock leaf"
/clone_lib="HL (Lolium multiflorum)"

ORIGIN

Alignment Scores:

Pred. No.: 4.26e-53 Length: 603
Score: 547.00 Matches: 108
Percent Similarity: 69.31% Conservative: 32
Best Local Similarity: 53.47% Mismatches: 58
Query Match: 23.20% Indels: 4
DB: 1 Gaps: 2

US-10-089-364-4 (1-449) x AU248054 (1-603)

QY 224 ArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeuMet 243
Db 3 AGATTAGAGAAAACCTGGCCGCGACAGAAATTTCCCGGAGCAGACAAATTCACATCATG 62
QY 244 AspMetCysSerPheAspThrThrLeuValAspThrThrLeuSerProphe 263
Db 63 GACCTTGTCCGTTTGATACCATTTGCTAATGAA-----CAAGGAGAGCTCTCTCCATT 116
QY 264 CysAspLeuPheThrHisAspGluTrpIleAsnTyrAspThrLeuGlnSerLeuLys 283
Db 117 TGCCACATATTCACTGCCCTCTGAATGCGCGCTACGATTACTACCAACAGTTGGAAG 176
QY 284 TyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAlaAsn 303
Db 177 TACTACGGCTATTTCATGGGGTAATCCACTCGGACCACTTCAGGGGTCGGTTTACTAAT 236
QY 304 GluLeuIleAlaArgLeuThrHisSerProValHisAspThrSerSerAsnHisThr 323
Db 237 GAGCTAATTGACGACTACTCGCTCTCCCGTCATCGATCAGACGACCTAATACACA 296
QY 324 LeuAspSerSerProAlaThrPheProLeuAsnSer-----ThrLeuTyrAlaAspPhe 341
Db 297 CTCGACCAACAATCCCGAGGAGTTTCTCTCGATAGCAAACTGCTTTACCGACATT 356
QY 342 SerHisAspAsnGlyIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLys 361
Db 357 AGCCACGACAAACGACCTACTAGCATATTGGCTGCGATGTTCTCTACAAAATTTCTCG 416
QY 362 ProLeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrp 381
Db 417 CCACTCTCAAGACGAGGTCCTAATTTTAAAGGAGCTGACGACTATTCGACTAGCCGT 476
QY 382 ThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlu 401
Db 477 ACTGTACCGTTTCGGTGGCGGTATCTATTTCGAAATTTGAAGTGCACAGATGACGGA 536
QY 402 ProLeuValArgValLeuValAsnAspArgValProLeuHisGlyCysProValAsp 421
Db 537 GATATGATACGATATTGTGAATGATCGCGTCTCTTCACTTCAATCCTGTGGCGAGAT 596
QY 422 AlaLeu 423
Db 597 GCATTG 602

RESULT 9
CD031252
LOCUS
DEFINITION mgmt005xe03.f 620 bp mRNA linear EST 07-MAY-2003
VERSION mgmt005xe03.5, mRNA sequence.
ACCESSION CD031252
KEYWORDS CD031252.1 GI:30413088
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.

REFERENCE

1 (bases 1 to 620)

AUTHORS

Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,

TITLE

Bhatterai,K. and Dean,R.A.

JOURNAL

COMMENT

Expressed sequence tags from the rice blast fungus, Magnaporthe
grisea
Unpublished (2002)
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu

Chromatogram file of this sequence is available, see contact
person,Best nr hit (April. 22, 2003) gb|AAB52508.1| phytase
[Thielavia heterothallica] 239 3e-62

PCR Primers

FORWARD: T3 primer

BACKWARD: T7 primer

Plate: mgmt005 row: E column: 03

Seq primer: T3

FEATURES

source

Location/Qualifiers
1..620
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="4091-5-8 X 4136-4-3"
/db_xref="taxon:148305"
/clone="mgmt005xe03"
/sex="Mat1-2 and Mat1-1 mixed culture"
/cell_type="mixed sexual development"
/dev_stages="asci, ascospores, perithecia, mycelium"
/clone_lib="Mated culture"
/note="Vector: pBluescriptSK; Site_1: EcoRI; Site_2: XhoI;
Two mating types were co-cultivated over a filter paper on
oatmeal agar medium. After three days at 25 C plates were
transferred to 21 C. Perithecia with asci and ascospores
formed at the beginning of the third week. Material was
collected by scraping tissue from the filter paper.
Sequences were processed by one of two methods. Where a
full-length alignment to the M. grisea genome sequence was
available, the EST sequence was trimmed according to the
alignment, otherwise sequence quality was assessed using
phredPhrap version 991019 and trimmed according to phd
files (0.05) and for vector seqs."

ORIGIN

Alignment Scores:

Pred. No.: 9.69e-49 Length: 620
Score: 510.00 Matches: 98
Percent Similarity: 64.39% Conservative: 34
Best Local Similarity: 47.80% Mismatches: 69
Query Match: 21.63% Indels: 4
DB: 6 Gaps: 2

US-10-089-364-4 (1-449) x CD031252 (1-620)

QY 190 AsnThrLeuAspProGlyThrCysThrValPheGluAspSerGluLeuAlaAspThrVal 209
Db 2 AACACGCTAAACCATACCTATGTACTTCTGAGAACACCAACTCGCAAGGAAGCC 61
QY 210 GluAlaAsnPheThrAlaThrPheValProSerIleArgGlnArgLeuGluAsnAspLeu 229
Db 62 CAAAAGAGTTATGGAGAGTGCCATGGCGGCATTAACAGAGCGCTTGAACACAGCGCTG 121
QY 230 SerGlyValThrLeuThrAspThrGluValThrTyrLeuMetAspMetCysSerPheAsp 249
Db 122 GAGGTGCAAACTTCACGACCAACGCGGTGAGATCATGGAGCTCTGCCCGTTTACG 181
QY 250 ThrIleSerThrSerThrValAspThrLysLeuSerPropheCysAspLeuPheThrHis 269
Db 182 ACCGTGGCAGATCCC-----CAAGCCACCCTGTCGAGATTCTGCACGCTGTTTACGCA 235
QY 270 AspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLysTyrTyrGlyHisGlyAla 289

oatmeal agar medium. After three days at 25 C plates were transferred to 21 C. Perithecia with asci and ascospores formed at the beginning of the third week. Material was collected by scraping tissue from the filter paper. Sequences were processed by one of two methods. Where a full-length alignment to the M. grisea genome sequence was available, the EST sequence was trimmed according to the alignment, otherwise sequence quality was assessed using phredPhrap version 91019 and trimmed according to phd files (0.05) and for vector seqs."

ORIGIN

Alignment Scores: 8.4e-42 Length: 586
Pred. No.: 450.50 Matches: 90
Score: 450.50
Percent Similarity: 68.55% Conservative: 19
Best Local Similarity: 56.60% Mismatches: 48
Query Match: 19.11% Indels: 3
DB: 6 Gaps: 1

US-10-089-364-4 (1-449) x CD030240 (1-586)

QY 292 ProLeuGlyProThrGlnGlyValGlyTyrAlaAsnGluLeuIleAlaArgLeuThrHis 311
Db 586 CCCTGGGCTCCACGCAAGGGGTGGGTGGTTCACGAGCTCATCGGAGGTTCG--TCA 529
QY 312 SerProValHisAspAspThrSerSerAsnHisThrLeuAspSerSerProAlaThrPhe 331
Db 528 AAGGCGTTGAAGGCCACACAAATACCACTCGACGCTCGACAGCAGCCATCGACGTTTC 469
QY 332 ProLeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSerIleLeu 351
Db 468 CCCTAGACAAAAAGCTGTACGCGGCTTTAGCCCATGATAACGATATGCTGGGCATCTAC 409
QY 352 PheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrThrThrValGlu---- 369
Db 408 GCCGCGCTGGGGATTTACAAACGCCGCCCGCCGATTCGGTCCCCAAAAAGAAAGG 349
QY 370 AsnIleThrGlnThrAspGlyPheSerSerAlaTrpThrValProPheAlaSerArgLeu 389
Db 348 AGCGCGCAGAGCTCAGCGGGTCTCTGTCAGCTGGCGGTACCGTTCCGACGAGGATG 289
QY 390 TyrValGluMetMetGlnCysGlnAlaGluGlnGluProLeuValArgValLeuValAsn 409
Db 288 TTTGTTCAAAAAATGACTTCGCGAGGCGCAGAACGAGGAGCTTGTGAGAACTCTCGTCAAC 229
QY 410 AspArgValValProLeuHisGlyCysProValAlaLeuGlyArgCysThrArgAsp 429
Db 228 GACAGGCTGACCGCGCTGCAGAACTGCGATGCCGACAGTAGTGGTCTGTTGCACGCTGAGC 169
QY 430 SerPheValArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAlaGluCysPhe 448
Db 168 AAGTTCGTTGAGAGCTTAAGCTTTGCGAGGAGTGGAGGTGCTGGGATCAATGTTTT 112

RESULT 11

BQ142672

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ142672 650 bp mRNA linear EST 24-APR-2002
6 Metarhizium anisopliae sf. acridum ARSEF 324 Metarhizium
anisopliae var. acridum cDNA, mRNA sequence.

BQ142672.1 GI:20279731

EST.

Metarhizium anisopliae var. acridum

Metarhizium anisopliae var. acridum

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Clavicipitaceae; mitosporic

Clavicipitaceae; Metarhizium.

1 (bases 1 to 650)

Freimoser, F.M., Screen, S., Baga, S., Hu, G. and St. Leger, R.J.

EST analysis of genes expressed by two different insect pathogenic

fungi during optimized secretion of proteins

Unpublished (2002)

Contact: Freimoser F. M.

Db 236 CGAGACTGGAGGCATATGATCTCCAGACACTGGGAGGTGATGTTACGCAAT 295
QY 290 GlyAsnProLeuGlyProThrGlnGlyValGlyTyrAlaAsnGluLeuIleAlaArgLeu 309
Db 296 GGCACACCCCTGGGCTCCACGCAAGGGGTGGGTGGTTCACGAGCTCATCGGAGGCTG 355
QY 310 ThrHisSerProValHisAspAspThrSerSerAsnHisThrLeuAspSerSerProAla 329
Db 356 CTCACAAAAGCCGTTGAAGACCCACAAATACCACTCGACGCTCGACGAGCCCATCG 415
QY 330 ThrPheProLeuAsnSerThrLeuTyrAlaAspPheSerHisAspAsnGlyIleIleSer 349
Db 416 ACCTGTCCTACACAAAAAGCTGACGCGCTTTAGCCATGATACGATATGCTGGGC 475
QY 350 IleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysProLeuSerThrThrThrValGlu 369
Db 476 ATCTAGCGCGCGCTGGGGATTACACGCCACGCGCCCGCGATTCGGTCCCCAAAAAGAG 535
QY 370 -----AsnIleThrGlnThrAspGlyPheSerSerAlaTrpThrValProPheAlaSer 387
Db 536 AGAAGAGCGCGGAGGAGCTCAGCGGCTTCTCGCCAGCTGGCGGTACCGTCCGACGCG 595
QY 388 ArgLeuTyrValGlu 392
Db 596 AGGATGTTGGTGAA 610

RESULT 10

CD030240/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CD030240 586 bp mRNA linear EST 07-MAY-2003
mgmt001x016f.b Mated culture Magnaporthe grisea cDNA clone
mgmt001x016 5', mRNA sequence.

CD030240

CD030240.1 GI:30412076

EST.

Magnaporthe grisea (anamorph: Pyricularia grisea)

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetes; incertae sedis; Magnaportheaceae; Magnaporthe.

1 (bases 1 to 586)

Ebbels, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,

Bhatterai, K. and Dean, R.A.

Expressed sequence tags from the rice blast fungus, Magnaporthe

grisea

Unpublished (2002)

Contact: Ebbels DJ

Department of Plant Pathology & Microbiology

Texas A&M University

Peterson Bldg, MS2132, College Station, TX 77843-2132, USA

Tel: 979 845 4831

Fax: 979 845 6483

Email: d-ebbles@tamu.edu

Chromatogram file of this sequence is available, see contact

person; Best nr hit (April. 22, 2003) gb|AAB52508.1| phytase

[Thielavia heterothallica] 166 5e-44

PCR Primers

FORWARD: T3 primer

BACKWARD: T7 primer

Plate: mgmt001 row: 0 column: 16

Seq primer: T3.

Location/Qualifiers

1. 586

/organism="Magnaporthe grisea"

/mol_type="mRNA"

/strain="4091-5-8 X 4136-4-3"

/db_xref="taxon:148305"

/clone="mgmt001x016"

/sex="Mat1-2 and Mat1-1 mixed culture"

/cell_type="mixed sexual development"

/dev_stage="asci, ascospores, perithecia, mycelium"

/clone_lib="Mated culture"

/note="Vector: pBluescriptSK; Site_1: EcoRI; Site_2: XhoI;

Two mating types were co-cultivated over a filter paper on


```

QY 386 AlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluProLeuValArg 405
Db 302 GTGCGCCGATGACGTGGAGAGATGACGTGACGGCTCGACGAGCGCTGGTGGCG 243
QY 406 ValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAlaLeuGlyArg 425
Db 242 ATCATCTCAACGACCGCGTGGTGGCGATCGGACGCTGCAACTCGGATCGACTGGGCGG 183
QY 426 CysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGlyAspTrpAla 445
Db 182 TGAAGCTGGGTGCTTTATTGATAGCTTACGCTGACGTTGTGCGCGCGGAGGCTGTGAAT 123
QY 446 GluCys 447
Db 122 CAGTGT 117

RESULT 13
AJ274007
LOCUS
DEFINITION
AJ274007 581 bp mRNA linear EST 29-DEC-1999
cDNA clone Ma#1628, mRNA sequence.
ACCESSION
AJ274007.1 GI:6433380
VERSION
AJ274007.1
KEYWORDS
Metarhizium anisopliae
SOURCE
Metarhizium anisopliae
ORGANISM
Metarhizium anisopliae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocremetidae; Hypocremetidae; Clavicipitaceae; mitosporic
Clavicipitaceae; Metarhizium.
REFERENCE
1 (bases 1 to 581)
Screen, S.E., Mathur, P. and St. Leger, R.J.
EST analysis of the insect pathogenic fungus Metarhizium anisopliae
TITLE
EST analysis of the insect pathogenic fungus Metarhizium anisopliae
JOURNAL
Unpublished (1999)
COMMENT
Contact: Screen SE
Entomology
University of Maryland
4112 Plant Sciences Building, College Park, MD 20742, USA.
FEATURES
source
1..581
Location/Qualifiers
/organism="Metarhizium anisopliae"
/mol_type="mRNA"
/strain="ARSEF 2575"
/db_xref="taxon:5530"
/clone="Ma#1628"
/clone_lib="Metarhizium anisopliae ARSEF 2575"
/notes="Vector: Unizap; Metarhizium anisopliae was grown on
insect cuticle for 24 hours. A cDNA library was
constructed in the unidirectional Lambda vector, Unizap"
ORIGIN
source
Alignment Scores:
Pred. No.: 2.31e-34 Length: 581
Score: 387.00 Matches: 73
Percent Similarity: 65.22% Conservative: 32
Best Local Similarity: 45.34% Mismatches: 54
Query Match: 16.41% Indels: 2
DB: 1 Gaps: 2

US-10-089-364-4 (1-449) x AJ274007 (1-581)

QY 7 SerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCysPheSerGluThr 26
Db 94 GCGGAGATCGATCAGCTCCAGTCATCGCTTAACACGGCTCTCGACCCACGATTTT 153
QY 27 SerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGluSerValIleSer 46
Db 154 CGCAAGCACTGGGCGCTACTCGCGTACTTCTCA--GCACACACAGGGGATCTATTAA 210
QY 47 ProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyVal 66
Db 211 CTTGATCCCGCTCGGATGCGAGTCACTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 270
QY 67 ArgTyrProThrAspSerIysGlyIysIysTyrSerAlaLeuIleGluGlnIleGln 86

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Db 271 CGCAACCCGACGCGCGCAAGTCCAAAGCGCTTACAGGACCTGTTGAGCGGATCCAAAA 330
QY 87 AsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsnTyrSerLeuGly 106
Db 331 GACGTCAAGACGATATGGGAGGCTTCGAGTTTCTCAAGATTACAGTTATCTCTAGGT 390
QY 107 AlaAspLeuThrProPheGlyGluGlnGluValAsnSerGlyIleLysPheTyr 126
Db 391 TCTGACGACCTCACCCCTTGGCGGACGAGGAATGTCAGTCTGAAAAAGTTCTTC 450
QY 127 GlnArgTyrGluSerLeuThrArgAsnIleVal---ProPheIleArgSerSerGlySer 145
Db 451 AAGCGCTATCAGAAGTTAGCGGAGGATTCGACCCATCCCTTGTTCGAGCTCGGGCTCT 510
QY 146 SerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLys 165
Db 511 GAAAGAGTGTGTCATGTCAGCGCAAGATTGTTTCATGCTTCTACAAAGCAAGGCAAG 570
QY 166 Asp 166
Db 571 AAT 573

RESULT 14
CN808226 1059 bp mRNA linear EST 27-MAY-2004
LOCUS
DEFINITION
CN808226 Metarhizium anisopliae ARSEF 2575 from insect blood
Metarhizium anisopliae cDNA clone B688 5', mRNA sequence.
ACCESSION
CN808226.1 GI:47729699
VERSION
CN808226.1
KEYWORDS
Metarhizium anisopliae
SOURCE
Metarhizium anisopliae
ORGANISM
Metarhizium anisopliae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocremetidae; Hypocremetidae; Clavicipitaceae; mitosporic
Clavicipitaceae; Metarhizium.
REFERENCE
1 (bases 1 to 1059)
Wang, C.S., Hu, G. and St. Leger, R.J.
Gene expression profiling of Metarhizium anisopliae grown under
different conditions: mechanisms of fungal opportunism
TITLE
Unpublished (2004)
JOURNAL
Contact: Wang CS
Department of Entomology
University of Maryland
4112 Plant Sciences Building, College Park, MD 20742, USA
Email: cwang4@umd.edu
Seq primer: M13 Reverse.
FEATURES
source
1..1059
Location/Qualifiers
/organism="Metarhizium anisopliae"
/mol_type="mRNA"
/db_xref="taxon:5530"
/clone="B688"
/clone_lib="Metarhizium anisopliae ARSEF 2575 from insect
blood"
/notes="Vector: pCMV.SPORT6.1; Metarhizium anisopliae was
grown in insect haemolymph for 24 hours. A cDNA library
was constructed in the vector pCMV.SPORT6.1"
ORIGIN

```

```

Alignment Scores:
Pred. No.: 5.9e-34 Length: 1059
Score: 387.00 Matches: 73
Percent Similarity: 65.22% Conservative: 32
Best Local Similarity: 45.34% Mismatches: 54
Query Match: 16.41% Indels: 2
DB: 7 Gaps: 2

US-10-089-364-4 (1-449) x CN808226 (1-1059)

QY 7 SerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCysPheSerGluThr 26
Db 372 GCGGAGATCGATCAGCTCCAGTCATCGCTTAACACGGCTCTCTGACCCACGATTTT 431

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QY 27 SerHisLeuTrpGlyGlnTyrAlaProPheSerLeuAlaAsnGluSerValIleSer 46
DB 432 CCACAGCACTGGGGCCAGTACTCGCGTACTTCTCA---GCACACAAGGATCTATTAG 488
QY 47 ProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSerArgHisGlyAla 66
DB 489 CTTGACATCCCGTCGGATGCGAGGTACCTTTGTTCAATCTGTCTCGACATGGGTCC 548
QY 67 ArgTyrProThrAspSerIlysglyllystyrSerAlaLeuIleGluLileGln 86
DB 549 CGCAACCCGAGCGCGCAAGTCCAAAGGCTTCAAGGACCTGTGAGCGGATCCAAAAA 608
QY 87 AsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsnTyrSerLeuGly 106
DB 609 GAGCTCAGGACTATGGGAAGGGCTCGAGTTCTCAAGATTACAGTACTACTAGT 668
QY 107 AlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGlyIleLysPheTyr 126
DB 669 TCTGACGACCTCACCCCTTGGCGGAGCAGGAATGGTCAAGTCTGGAAAAAAGTTCTTC 728
QY 127 GlnArgTyrGluSerLeuThrArgAsnIleVal---ProPheIleArgSerSerGlySer 145
DB 729 AAGCGCTATCAGAAAGTATGCGGAGGATTCGACCCATCCCTTTGTTTCGAGCCCTCGGCTCT 788
QY 146 SerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThrLysLeuLys 165
DB 789 GAAAGAGTGTGATCTACGCGCAAGATTTGTTCATGCTTCTACAGGCCAAGCGCAG 848
QY 166 Asp 166
DB 849 AAT 851

RESULT 15
AQ255459
LOCUS
DEFINITION
  mgxb0014M15r CUGI Rice Blast BAC Library Magnaporthe grisea genomic
  clone mgxb0014M15r, genomic survey sequence.
ACCESSION
  AQ255459
VERSION
  AQ255459.1 GI:3779774
KEYWORDS
  GSS.
SOURCE
  Magnaporthe grisea (anamorph: Pyricularia grisea)
  Magnaporthe grisea
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
  Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
  1 (bases 1 to 837)
AUTHORS
  Yu, Y.; Zhu, H.; Boyd, C.A.; Gaudette, B.; Gayle, A.; Kingsbury, R.;
  Phillips, K.; Sasinowski, M.; Wing, R.A. and Dean, R.A.
TITLE
  A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
  Genome
JOURNAL
  Unpublished (1998)
COMMENT
  Contact: Dean RA
  Clemson University Genomics Institute
  100 Jordan Hall, Clemson University, Clemson, SC 29634
  Tel.: 864 656 5737
  Fax: 864 656 4293
  Email: rdean@clemson.edu
  Seq primer: GGAACAGCTATGACCATG
  Class: BAC ends
  High quality sequence start: 60
  High quality sequence stop: 277.
FEATURES
  Location/Qualifiers
    1..837
      /organism="Magnaporthe grisea"
      /mol_type="genomic DNA"
      /strain="70-15"
      /db_xref="taxon:148305"
      /clone="mgxb0014M15r"
      /tissue_type="Protoplasts"
      /lab_host="E. coli DH10B"
      /clone_lib="CUGI Rice Blast BAC Library"
      /note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;"

```

Rice blast is one of the most devastating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."

ORIGIN

```

Alignment Scores:
Pred. No.: 1,19e-32 Length: 837
Score: 374.50 Matches: 80
Percent Similarity: 55.67% Conservative: 28
Best local Similarity: 41.24% Mismatches: 69
Query Match: 15.88% Indels: 17
DB: 8 Gaps: 2

US-10-089-364-4 (1-449) x AQ255459 (1-837)
QY 223 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 242
DB 124 CAACGCATAGGCTGGGATTTTCAAGGTGCTGGGTTAACGGTCAAGACGTTGTAATCTT 183
QY 243 MetAspMetCysSerPheAspThrThrIleSerThrSerThrValAspThrLysLeuSerPro 262
DB 184 ATGGGACTGTGCACCATGGAAACAACGGCGAATCTTTGAAAAAATCTGGCCAACTTTACCGG 243
QY 263 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 282
DB 244 CTTTGCAATCTGTTTACGGAACGACATGGGTAATAATATGGTTACTTGTCCACGCTGCAA 303
QY 283 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 302
DB 304 AAATGGTACAGATACGGAACGGTAATCTTTGGGCCCAACTATGGCGCTGGGATGGGTA 363
QY 303 AsnGluLeuIleAlaGluLeuThrHisSerProValHisAspAspThrSerSerAsnHis 322
DB 364 AACGAACCTTATGTCACGATTAAACCGAAGCCGACGTCACCAAGATCAACCATGTCCAATACG 423
QY 323 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 342
DB 424 ACACCTTGACATGAACCCGGAACCTTACTCTACAGGCAAAATTCATGCTGATTTATC 483
QY 343 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsn----- 358
DB 484 CATACGGACGATATTATAGGATTTACGCCGCGTTGGGCTATTTAACGCCCGCGCTTT 543
QY 359 GlyThrLysProLeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSer 378
DB 544 GGAAAAACAAAAATTTCCACCTATAAAATTCACATCCATAGGAGCTTGGTGGATTTTAT 603
QY 379 SerAlaTrpThrValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAla 398
DB 604 TCA-----ATATGAGATGCCCATTTG 624
QY 399 GluGlnGluProLeuValArgValLeuValAsnAspArgVal 412
DB 625 GGGCTAGAGATGTCGTTGAGAAAAATAATTTTCATCGGACATA 666

```

Search completed: October 24, 2004, 17:23:20
Job time : 5518 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 24, 2004, 11:03:13 ; Search time 115 Seconds

(without alignments)
1400.604 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

Sequence: 1 MLAVPASRNQSSCDTVDQY.....SFVRGLSFARSGDWAECFA 449

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Genesep23sep04:*
- 2: Genesep1980s:*
- 3: Genesep1990s:*
- 4: Genesep2000s:*
- 5: Genesep2001s:*
- 6: Genesep2002s:*
- 7: Genesep2003as:*
- 8: Genesep2003bs:*
- 9: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	2358	100.0	449	4	AA72974	Aspergill
2	2358	100.0	482	4	AA72978	Aspergill
3	2353	99.8	448	5	ABB83811	Carrot ex
4	2353	99.8	467	2	AA113333	Aspergill
5	2353	99.8	467	2	AA113333	Aspergill
6	2353	99.8	467	2	AA113333	Aspergill
7	2353	99.8	467	2	AA113333	Aspergill
8	2353	99.8	467	2	AA113333	Aspergill
9	2350	99.7	467	8	ADL91242	Aspergill
10	2350	99.7	467	8	ADL91242	Aspergill
11	2349	99.6	467	8	ADL91262	Mutant ph
12	2349	99.6	467	8	ADL91260	Mutant ph
13	2349	99.6	467	8	ADL91264	Mutant ph
14	2349	99.6	467	8	ADL91274	Mutant ph
15	2349	99.6	467	8	ADL91248	Mutant ph
16	2347	99.5	467	8	ADL91258	Mutant ph
17	2347	99.5	467	8	ADL91272	Mutant ph
18	2347	99.5	467	8	ADL91270	Mutant ph
19	2347	99.5	467	8	ADL91256	Mutant ph
20	2346	99.5	467	8	ADL91245	Mutant ph
21	2346	99.5	467	8	ADL91266	Mutant ph
22	2346	99.5	467	8	ADL91266	Mutant ph
23	2345	99.4	467	8	ADL91280	Mutant ph
24	2345	99.4	467	8	ADL91282	Mutant ph
25	2343	99.4	467	8	ADL91276	Mutant ph
					ADL91309	Mutant ph

ALIGNMENTS

RESULT 1

AA72974

ID AA72974 standard; protein; 449 AA.

AC AA72974;

XX

DT 13-JUN-2001 (first entry)

DE Aspergillus niger phytase (Phy) A-1 protein.

XX

Phytase A; Phy; plant productivity; phosphorus utility;

biomass production; hypocotyl production; epicotyl production;

transgenic plant; phytate.

OS Aspergillus niger.

XX

PN WO200122806-A1.

XX

PD 05-APR-2001.

XX

PF 22-SEP-2000; 2000WO-AU001183.

XX

PR 24-SEP-1999; 99AU-00003049.

XX

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX

PA (AUWO-) AUSTRALIAN WOOL RES & PROMOTION ORG.

XX

PI

XX

DR

XX

DR

XX

XX

PT

XX

PT

XX

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

Adl91278 Mutant ph
Adl91284 Mutant ph
Aar14360 Phytase.
Adl91292 Mutant ph
Adl91290 Mutant ph
Adl91294 Mutant ph
Adl91286 Mutant ph
Adl91288 Mutant ph
Adf43251 Aspergill
Adl91296 Mutant ph
Aay69548 Aspergill
Aab20505 Aspergill
Aab173070 Aspergill
Aar46792 Phytase.
Aar46234 A. niger
Aay69547 Aspergill
Aab20504 Aspergill
Adl73069 Aspergill
Aay69546 Aspergill
Aab20503 Aspergill

26 2343 99.4 467 8 ADL91278
27 2342 99.3 467 8 ADL91284
28 2341 99.3 467 2 AAR14360
29 2341 99.3 467 8 ADL91292
30 2340 99.3 467 8 ADL91290
31 2340 99.2 467 8 ADL91294
32 2339 99.2 467 8 ADL91286
33 2339 99.2 467 8 ADL91288
34 2334 99.0 444 8 ADF43251
35 2327 98.7 467 8 ADL91296
36 2321 98.4 441 3 AAY69548
37 2321 98.4 441 3 AAB20505
38 2321 98.4 441 8 ADL73070
39 2309 97.9 467 2 AAR46792
40 2309 97.9 467 2 AAR46234
41 2291 97.2 441 3 AAY69547
42 2288 97.0 441 8 AAB20504
43 2288 97.0 441 8 ADL73069
44 2277 96.6 441 3 AAY69546
45 2277 96.6 441 3 AAB20503

The invention relates to a method of modifying plant productivity which involves expressing (Phy) A phytase gene from *Aspergillus niger*, in a plant cell. Phytase gene is capable of facilitating plants ability to utilise soil phosphorus. It is used to enhance the phosphorus nutrition of a plant or the growth of a plant on a phosphorus source comprising phytate and/or increase the phosphorus content of a plant. This gene is used to enhance the biomass produced by a plant and also to enhance the rate of hypocotyl production or the rate of epicotyl production. Transgenic plant containing phytase gene has improved productivity than its isogenic counterparts. The present sequence is *Aspergillus niger* Phy

CC	A-1 protein
XX	Sequence 449 AA;
SQ	
	Query Match 100.0%; Score 2358; DB 4; Length 449;
	Best Local Similarity 100.0%; Pred. No. 5.6e-216;
	Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MLAVPASRNQSSCDTVDQGQCSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFPAQV 60
DB	1 MLAVPASRNQSSCDTVDQGQCSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFPAQV 60
QY	61 LSRHGARYPTDSKGGKYSALIEEQONATTFDGKYAFKTYNYSLGADDLTPFGEQELVN 120
DB	61 LSRHGARYPTDSKGGKYSALIEEQONATTFDGKYAFKTYNYSLGADDLTPFGEQELVN 120
QY	121 SGIKFYORYESLTRNIIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAGQSSPKIDV 180
DB	121 SGIKFYORYESLTRNIIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAGQSSPKIDV 180
QY	181 VISEASSNNLLDPGCTCVFDSELDVNEAFTVFPSRQRLENLDSGVTLTDTEVT 240
DB	181 VISEASSNNLLDPGCTCVFDSELDVNEAFTVFPSRQRLENLDSGVTLTDTEVT 240
QY	241 YLMDCSFDTTISTSTVDTKLSPPFCDLFTHDEWINDYQLSKKKYYGHGAGNPLGTQGVG 300
DB	241 YLMDCSFDTTISTSTVDTKLSPPFCDLFTHDEWINDYQLSKKKYYGHGAGNPLGTQGVG 300
QY	301 YANELIARLTSPVHDDTSSNHTLSDSPATPFLNSTLYADFSDHNGIIISILFALGLYNGT 360
DB	301 YANELIARLTSPVHDDTSSNHTLSDSPATPFLNSTLYADFSDHNGIIISILFALGLYNGT 360
QY	361 KPLSTTTVENITQTDFGSSAWTVFPASRLYVEMMOCQAQEPLVRVLVNDRVVPLHGCPV 420
DB	361 KPLSTTTVENITQTDFGSSAWTVFPASRLYVEMMOCQAQEPLVRVLVNDRVVPLHGCPV 420
QY	421 DALGRCTRDSFVRGLSFARSGGDWAECPA 449
DB	421 DALGRCTRDSFVRGLSFARSGGDWAECPA 449
	RESULT 2
ID	AAV72978 standard; protein; 482 AA.
XX	AAV72978;
AC	AAV72978;
XX	
DT	11-SEP-2003 (revised)
DT	13-JUN-2001 (first entry)
XX	
DE	Carrot extensin leader peptide-A. niger phytase A-1 chimeric protein.
XX	
KW	Phytase A; Phy; plant productivity; phosphorus utility;
KW	biomass production; hypocotyl production; epicotyl production;
KW	transgenic plant; phytate; carrot; extensin.
XX	
OS	Daucus carota.
OS	Aspergillus niger.
OS	Chimeric.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..33 Carrot_extensin_leader_peptide
FT	34..482 Mature_carrot_extensin_leader_peptide-A.
FT	niger_phytase_A-2_chimeric_protein
XX	
PN	WO200122806-A1.
XX	
PD	05-APR-2001.
XX	
PB	22-SEP-2000; 2000WO-AU001183.
XX	
.XX	

PR	24-SEP-1999; 99AU-00003049.
XX	(CSIR) COMMONWEALTH SCI & IND RES ORG.
PA	(AUWO-) AUSTRALIAN WOOL RES & PROMOTION ORG.
XX	
PI	Richardson AE, Hayes JE, Simpson RJ;
XX	
DR	WPI; 2001-244964/25.
DR	N-PSDB; AAD03287.
XX	
PT	New isolated nucleic acid encoding a mature phytase polypeptide for
PT	enhancing the phosphorus nutrition of a plant, the growth of a plant on a
PT	phosphorus source and the phosphorus content of a plant.
XX	
PS	Claim 10; Fig 2; 144pp; English.
XX	
CC	The invention relates to a method of modifying plant productivity which
CC	involves expressing phytase (phy) A gene from Aspergillus niger, in a
CC	plant cell. Phytase gene is capable of facilitating plants ability to
CC	utilise soil phosphorus. It is used to enhance the phosphorus nutrition
CC	of a plant or the growth of a plant on a phosphorus source comprising
CC	phytate and/or increase the phosphorus content of a plant. This gene is
CC	used to enhance the biomass produced by the rate of epicotyl production.
CC	rate of hypocotyl production or the rate of epicotyl production.
CC	Transgenic plant containing phytase gene has improved productivity than
CC	its isogenic counterparts. The present sequence is carrot extensin leader
CC	peptide-A. niger phytase A-1 chimeric protein. This chimeric protein is
CC	used to enhance phosphorus nutrition in plants. (Updated on 11-SEP-2003
CC	to standardise OS field)
XX	
SQ	Sequence 482 AA;
	Query Match 100.0%; Score 2358; DB 4; Length 482;
	Best Local Similarity 100.0%; Pred. No. 6.3e-216; Indels 0; Gaps 0;
	Matches 449; Conservative 0; Mismatches 0;
QY	1 MLAVPASRNQSSCDTVDQGQCSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFPAQV 60
DB	34 MLAVPASRNQSSCDTVDQGQCSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFPAQV 93
QY	61 LSRHGARYPTDSKGGKYSALIEEQONATTFDGKYAFKTYNYSLGADDLTPFGEQELVN 120
DB	94 LSRHGARYPTDSKGGKYSALIEEQONATTFDGKYAFKTYNYSLGADDLTPFGEQELVN 153
QY	121 SGIKFYORYESLTRNIIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAGQSSPKIDV 180
DB	154 SGIKFYORYESLTRNIIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAGQSSPKIDV 213
QY	181 VISEASSNNLLDPGCTCVFDSELDVNEAFTVFPSRQRLENLDSGVTLTDTEVT 240
DB	214 VISEASSNNLLDPGCTCVFDSELDVNEAFTVFPSRQRLENLDSGVTLTDTEVT 273
QY	241 YLMDCSFDTTISTSTVDTKLSPPFCDLFTHDEWINDYQLSKKKYYGHGAGNPLGTQGVG 300
DB	274 YLMDCSFDTTISTSTVDTKLSPPFCDLFTHDEWINDYQLSKKKYYGHGAGNPLGTQGVG 333
QY	301 YANELIARLTSPVHDDTSSNHTLSDSPATPFLNSTLYADFSDHNGIIISILFALGLYNGT 360
DB	334 YANELIARLTSPVHDDTSSNHTLSDSPATPFLNSTLYADFSDHNGIIISILFALGLYNGT 393
QY	361 KPLSTTTVENITQTDFGSSAWTVFPASRLYVEMMOCQAQEPLVRVLVNDRVVPLHGCPV 420
DB	394 KPLSTTTVENITQTDFGSSAWTVFPASRLYVEMMOCQAQEPLVRVLVNDRVVPLHGCPV 453
QY	421 DALGRCTRDSFVRGLSFARSGGDWAECPA 449
DB	454 DALGRCTRDSFVRGLSFARSGGDWAECPA 482
	RESULT 3
ID	ABB83811 standard; protein; 448 AA.
XX	ABB83811
.XX	

AC ABB83811;
 XX 17-SEP-2002 (first entry)
 XX Aspergillus niger phyA related polypeptide 2.
 DE Aspergillus niger; phytase; phyA; Pasteur Pichia; enzyme.
 KW Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; enzyme.
 XX Aspergillus niger.
 OS Aspergillus niger.
 XX CN133363-A.
 XX 30-JAN-2002.
 XX 12-JUL-2000; 2000CN-00117245.
 XX 12-JUL-2000; 2000CN-00117245.
 XX (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.
 XX Chen Z, Yang L, Fang L;
 DR WPI; 2002-305615/35.
 DR N-PSDB; ABN85590.
 XX Phytase gene sequence and application in yeast thereof.
 PT Disclosure; Fig 4; 48pp; Chinese.
 XX The invention relates to a coded phytase gene sequence suitable for
 CC secretion and expression in yeast and its application. It is mainly
 CC characterised by removing nucleotide sequence of +45-+146 bit from phyA
 CC total length structure gene sequence, removing Aspergillus niger signal
 CC peptide coded sequence of +1-+44 and +147-+159, connecting a part of
 CC signal peptide code sequence suitable for secretion and expression at 5'
 CC end and connecting a restriction endonuclease site at 3' end. The
 CC different carriers can be connected into said gene sequence so as to form
 CC a recombinant plasmid with different functions and after the recombinant
 CC plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia
 CC yeast, finally the invented Pasteur Pichia yeast engineering bacterium
 CC (CCTCC NO:M200005) can be obtained through the screening process. By
 CC using the invention, the industrial process of phytase bio-expression can
 CC be successfully implemented. The present sequence is that of a
 CC polypeptide of the invention
 XX Sequence 448 AA;
 SQ
 Query Match 99.8%; Score 2353; DB 5; Length 448;
 Best Local Similarity 100.0%; Pred. No. 1.7e-215;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPACGRVTFQVL 61
 DB 1 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPACGRVTFQVL 60
 QY 62 SRHGARYPTDSKGGKYSALIEEIQONATTPDGKYAFLKTYNSLGGDLTPFGQELVNS 121
 DB 61 SRHGARYPTDSKGGKYSALIEEIQONATTPDGKYAFLKTYNSLGGDLTPFGQELVNS 120
 QY 122 GIKFYQRYESTRNIVPFIRSSGSRVIAASKKIEGFQSTKLDPRAPQGSQSPKIDVV 181
 DB 121 GIKFYQRYESTRNIVPFIRSSGSRVIAASKKIEGFQSTKLDPRAPQGSQSPKIDVV 180
 QY 182 ISEASSNNLIDPCTCTVFEDSELADTVANFTATFVPSIRQLENDLSGVLTDTEVTV 241
 DB 181 ISEASSNNLIDPCTCTVFEDSELADTVANFTATFVPSIRQLENDLSGVLTDTEVTV 240
 QY 242 LMDMCSPTTISTVDTKLSGFCDLFTHDEWINYDYLQSLKYYGHGAGNPLGFTQGVY 301
 DB 241 LMDMCSPTTISTVDTKLSGFCDLFTHDEWINYDYLQSLKYYGHGAGNPLGFTQGVY 300
 QY 302 ANELIARLTHSPVHDDTSSNHTLSSPATPLNTLYADFSHNGIISILFALGLYNGTK 361
 DB 301 ANELIARLTHSPVHDDTSSNHTLSSPATPLNTLYADFSHNGIISILFALGLYNGTK 360
 QY 362 PLSTTTVENITQDGFSSAWTVPFASRLYVEMMQCOAQEPLVRLVNDRVVPLHGCPVD 421
 DB 361 PLSTTTVENITQDGFSSAWTVPFASRLYVEMMQCOAQEPLVRLVNDRVVPLHGCPVD 420
 QY 422 ALGRCRTDSFVRGLSFARSGGWAECFA 449
 DB 421 ALGRCRTDSFVRGLSFARSGGWAECFA 448
 RESULT 4
 AAR11333
 ID AAR11333 standard; protein; 467 AA.
 XX AAR11333;
 AC AAR11333;
 XX 25-MAR-2003 (revised)
 DT 30-MAR-2000 (revised)
 DT 31-MAY-1991 (first entry)
 XX Recombinant chromosomal phytase.
 DE Microbial phytase; animal feeds; inositol; inorganic phosphates.
 XX Synthetic.
 OS EP420358-A.
 XX 03-APR-1991.
 PD 27-SEP-1990; 90EP-00202565.
 PF 27-SEP-1989; 89EP-00202436.
 PR 17-AUG-1990; 90EP-0020231.
 XX (KONN) GIST-BROCADES NV.
 PA (STAM) DSM NV.
 PA Van Gorcom RF, Van Hartingsveldt W, Vanparidon PA, Beenstra AE;
 PI Luiten RG, Seltten GCM;
 XX WPI; 1991-095799/14.
 DR N-PSDB; AAQ11175.
 XX DNA encoding phytase - used for recombinant expression for prodn. of
 PT phytase for conversion of phytate to inositol and inorganic phosphate
 PT esp. in animal feed.
 XX Disclosure; Fig 8; 61pp; English.
 XX This sequence is encoded by a DNA sequence deduced from comparisons of
 CC respective sequences of clones identified using oligonucleotide probes.
 CC The use of recombinant DNA methods for the the enzyme prodn. allows the
 CC large scale prodn. of proteins and peptides having phytase activity.
 CC These are used for the conversion of phytate to inositol and inorganic
 CC phosphate and can be used in industrial processes. The phosphate content
 CC of manure thus can be decreased. See also AAQ11157-74. (Revised record
 CC issued to correct errors present in the sequence portion of the original
 CC GENESEQ entry.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on
 CC 25-MAR-2003 to correct PI field.)
 XX Sequence 467 AA;
 SQ
 Query Match 99.8%; Score 2353; DB 2; Length 467;
 Best Local Similarity 100.0%; Pred. No. 1.8e-215;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPACGRVTFQVL 61
 DB 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPACGRVTFQVL 79
 QY 62 SRHGARYPTDSKGGKYSALIEEIQONATTPDGKYAFLKTYNSLGGDLTPFGQELVNS 121

CC	to inositol and inorganic phosphate. It shows optimum activity at pH 5.5
CC	and 2.5, has a specific activity of about 100 U/mg and a mol.wt. of 85
CC	kDa (56.5 kDa unglycosylated). Its amino acid sequence was deduced from
CC	an isolated phytase cDNA clone (AAT65136). Isolation of this clone allows
CC	large-scale prodn. of the phytase in transformed host cells and used to
CC	prepare animal feed, reduce phytase levels in manure (by adding the
CC	enzyme to animal feed), and also to liberate inorganic phosphates from
CC	myoinositol phosphates in e.g. starch prodn. from cereals and soy
CC	processing. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-
CC	MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA
CC	field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 17-OCT-
CC	2003 to standardise OS field)
XX	
QQ	Sequence 467 AA;
	Query Match 99.8%; Score 2353; DB 2; Length 467;
	Best Local Similarity 100.0%; Pred. No. 1.8e-215; Indels 0; Gaps 0;
	Matches 448; Conservative 0; Mismatches 0;
QY	2 LAVPAGRNQSSCDTVQGYCFSETSHLWQYAPFFSLANESVISPVPAGCRVTFPAQVL 61
DB	20 LAVPASENQSSCDTVQGYCFSETSHLWQYAPFFSLANESVISPVPAGCRVTFPAQVL 79
QY	62 SRHGARYPTDSKGKYSALIEEIQONATTFDGKYAFILKTYNSILGADDLTPFGQELVNS 121
DB	80 SRHGARYPTDSKGKYSALIEEIQONATTFDGKYAFILKTYNSILGADDLTPFGQELVNS 139
QY	122 GIKFYQRYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLDPRAQPCQSSPKIDVV 181
DB	140 GIKFYQRYESLTRNIVPFISSGSSRVIASGKKFIEGFQSTKLDPRAQPCQSSPKIDVV 199
QY	182 ISEASSNNLTDPGCTCFVFDSELDATVEANFTATFVPSIRQRLNDLSGVTLTDTETVY 241
DB	200 ISEASSNNLTDPGCTCFVFDSELDATVEANFTATFVPSIRQRLNDLSGVTLTDTETVY 259
QY	242 LMDMCSFDTTSTVDTKLPFCDLFTHDEWINVDYQLSKKKYGHGAGNPLGPTQGVGY 301
DB	260 LMDMCSFDTTSTVDTKLPFCDLFTHDEWINVDYQLSKKKYGHGAGNPLGPTQGVGY 319
QY	302 ANELIARLTHSPVHDDTSSNHTLSSSPATFFPLNSTLYADFSDHNGIISILFALGLYNGTK 361
DB	320 ANELIARLTHSPVHDDTSSNHTLSSSPATFFPLNSTLYADFSDHNGIISILFALGLYNGTK 379
QY	362 PLSTTTVENITQTDGFSSAWTPVPASRLYVEMMQCAEQEPLRVLVNDRVVPLHGCPCVD 421
DB	380 PLSTTTVENITQTDGFSSAWTPVPASRLYVEMMQCAEQEPLRVLVNDRVVPLHGCPCVD 439
QY	422 ALGRCTRDSFVRGLSFARSGGDWAECEFA 449
DB	440 ALGRCTRDSFVRGLSFARSGGDWAECEFA 467
RESULT 6	
AAAY39904	
ID	AAAY39904 standard; protein; 467 AA.
XX	AAAY39904;
AC	
XX	
DT	07-DEC-1999 (first entry)
XX	
DE	A. ficum phytase protein sequence.
XX	
KW	Phytase; variant; enzyme; phosphorus liberation; phytase substrate;
KW	phytate level reduction; animal manure; food preparation; soy processing;
KW	inositol manufacture.
XX	
OS	Aspergillus ficum.
XX	
PN	W09949022-A1.
XX	
PD	30-SEP-1999.
XX	
PF	22-MAR-1999; 99WO-DK000153.

Db	80	SRHGARYPTDSKGYKYSALIEIQNATTFDGKYAFLEKTYNSLGADDLTPFGEQLVNS	139
Qy	122	GKFKQRYESLNRNIVPFFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAPQGGSSPKIDVV	181
Db	140	GKFKQRYESLNRNIVPFFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAPQGGSSPKIDVV	199
Qy	182	ISEASSNNLTDPGCTCTVFEDSELATVEANFTATVPFSIRQRLNDLSGVLTLDTEVY	241
Db	200	ISEASSNNLTDPGCTCTVFEDSELATVEANFTATVPFSIRQRLNDLSGVLTLDTEVY	259
Qy	242	LMDMCSFDIISTVTDKLSPPFCDLTFHDEWINDYLSLKKYKHGAGNPLGPTQGVY	301
Db	260	LMDMCSFDIISTVTDKLSPPFCDLTFHDEWINDYLSLKKYKHGAGNPLGPTQGVY	319
Qy	302	ANELIARLTHSPVHDDTSSNHTLDSPPATPLNLTLYADFSHDNGIISILFALGLYNGTK	361
Db	320	ANELIARLTHSPVHDDTSSNHTLDSPPATPLNLTLYADFSHDNGIISILFALGLYNGTK	379
Qy	362	PLSTTTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLRYVLVNDRVVPLHGCPVD	421
Db	380	PLSTTTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLRYVLVNDRVVPLHGCPVD	439
Qy	422	ALGCRTRDSFVRGLSFARSGGDWAECFA	449
Db	440	ALGCRTRDSFVRGLSFARSGGDWAECFA	467

Db	80	SRHGARYPTDSKGYKYSALIEIQNATTFDGKYAFLEKTYNSLGADDLTPFGEQLVNS	139
Qy	122	GKFKQRYESLNRNIVPFFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAPQGGSSPKIDVV	181
Db	140	GKFKQRYESLNRNIVPFFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAPQGGSSPKIDVV	199
Qy	182	ISEASSNNLTDPGCTCTVFEDSELATVEANFTATVPFSIRQRLNDLSGVLTLDTEVY	241
Db	200	ISEASSNNLTDPGCTCTVFEDSELATVEANFTATVPFSIRQRLNDLSGVLTLDTEVY	259
Qy	242	LMDMCSFDIISTVTDKLSPPFCDLTFHDEWINDYLSLKKYKHGAGNPLGPTQGVY	301
Db	260	LMDMCSFDIISTVTDKLSPPFCDLTFHDEWINDYLSLKKYKHGAGNPLGPTQGVY	319
Qy	302	ANELIARLTHSPVHDDTSSNHTLDSPPATPLNLTLYADFSHDNGIISILFALGLYNGTK	361
Db	320	ANELIARLTHSPVHDDTSSNHTLDSPPATPLNLTLYADFSHDNGIISILFALGLYNGTK	379
Qy	362	PLSTTTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLRYVLVNDRVVPLHGCPVD	421
Db	380	PLSTTTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLRYVLVNDRVVPLHGCPVD	439
Qy	422	ALGCRTRDSFVRGLSFARSGGDWAECFA	449
Db	440	ALGCRTRDSFVRGLSFARSGGDWAECFA	467

Db	80	SRHGARYPTDSKGYKYSALIEIQNATTFDGKYAFLEKTYNSLGADDLTPFGEQLVNS	139
Qy	122	GKFKQRYESLNRNIVPFFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAPQGGSSPKIDVV	181
Db	140	GKFKQRYESLNRNIVPFFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAPQGGSSPKIDVV	199
Qy	182	ISEASSNNLTDPGCTCTVFEDSELATVEANFTATVPFSIRQRLNDLSGVLTLDTEVY	241
Db	200	ISEASSNNLTDPGCTCTVFEDSELATVEANFTATVPFSIRQRLNDLSGVLTLDTEVY	259
Qy	242	LMDMCSFDIISTVTDKLSPPFCDLTFHDEWINDYLSLKKYKHGAGNPLGPTQGVY	301
Db	260	LMDMCSFDIISTVTDKLSPPFCDLTFHDEWINDYLSLKKYKHGAGNPLGPTQGVY	319
Qy	302	ANELIARLTHSPVHDDTSSNHTLDSPPATPLNLTLYADFSHDNGIISILFALGLYNGTK	361
Db	320	ANELIARLTHSPVHDDTSSNHTLDSPPATPLNLTLYADFSHDNGIISILFALGLYNGTK	379
Qy	362	PLSTTTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLRYVLVNDRVVPLHGCPVD	421
Db	380	PLSTTTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLRYVLVNDRVVPLHGCPVD	439
Qy	422	ALGCRTRDSFVRGLSFARSGGDWAECFA	449
Db	440	ALGCRTRDSFVRGLSFARSGGDWAECFA	467

Db	80	SRHGARYPTDSKGYKYSALIEIQNATTFDGKYAFLEKTYNSLGADDLTPFGEQLVNS	139
Qy	122	GKFKQRYESLNRNIVPFFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAPQGGSSPKIDVV	181
Db	140	GKFKQRYESLNRNIVPFFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAPQGGSSPKIDVV	199
Qy	182	ISEASSNNLTDPGCTCTVFEDSELATVEANFTATVPFSIRQRLNDLSGVLTLDTEVY	241
Db	200	ISEASSNNLTDPGCTCTVFEDSELATVEANFTATVPFSIRQRLNDLSGVLTLDTEVY	259
Qy	242	LMDMCSFDIISTVTDKLSPPFCDLTFHDEWINDYLSLKKYKHGAGNPLGPTQGVY	301
Db	260	LMDMCSFDIISTVTDKLSPPFCDLTFHDEWINDYLSLKKYKHGAGNPLGPTQGVY	319
Qy	302	ANELIARLTHSPVHDDTSSNHTLDSPPATPLNLTLYADFSHDNGIISILFALGLYNGTK	361
Db	320	ANELIARLTHSPVHDDTSSNHTLDSPPATPLNLTLYADFSHDNGIISILFALGLYNGTK	379
Qy	362	PLSTTTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLRYVLVNDRVVPLHGCPVD	421
Db	380	PLSTTTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLRYVLVNDRVVPLHGCPVD	439
Qy	422	ALGCRTRDSFVRGLSFARSGGDWAECFA	449
Db	440	ALGCRTRDSFVRGLSFARSGGDWAECFA	467

Db	80	SRHGARYPTDSKGYKYSALIEIQNATTFDGKYAFLEKTYNSLGADDLTPFGEQLVNS	139
Qy	122	GKFKQRYESLNRNIVPFFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAPQGGSSPKIDVV	181
Db	140	GKFKQRYESLNRNIVPFFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAPQGGSSPKIDVV	199
Qy	182	ISEASSNNLTDPGCTCTVFEDSELATVEANFTATVPFSIRQRLNDLSGVLTLDTEVY	241
Db	200	ISEASSNNLTDPGCTCTVFEDSELATVEANFTATVPFSIRQRLNDLSGVLTLDTEVY	259
Qy	242	LMDMCSFDIISTVTDKLSPPFCDLTFHDEWINDYLSLKKYKHGAGNPLGPTQGVY	301
Db	260	LMDMCSFDIISTVTDKLSPPFCDLTFHDEWINDYLSLKKYKHGAGNPLGPTQGVY	319
Qy	302	ANELIARLTHSPVHDDTSSNHTLDSPPATPLNLTLYADFSHDNGIISILFALGLYNGTK	361
Db	320	ANELIARLTHSPVHDDTSSNHTLDSPPATPLNLTLYADFSHDNGIISILFALGLYNGTK	379
Qy	362	PLSTTTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLRYVLVNDRVVPLHGCPVD	421
Db	380	PLSTTTVENITQDGFSSAWTVFPASRLYVEMMQCAEQEPLRYVLVNDRVVPLHGCPVD	439
Qy	422	ALGCRTRDSFVRGLSFARSGGDWAECFA	

XX 23-MAR-1998; 98DK-00000407.
 PR 19-JUN-1998; 98DK-00000806.
 PR 18-SEP-1998; 98DK-00001176.
 PR 22-JAN-1999; 99DK-00000091.
 XX (NOVO) NOVO-NORDISK AS.
 XX
 XX Svendsen A;
 PI
 XX WPI; 1999-580444/49.
 DR N-PSDB; AA227421.
 XX
 XX New variant phytase enzymes, used for liberating phosphorus from a
 PT phytase substrate, for reducing phytate levels in animal manure and in
 PT feed and food preparations.
 XX
 XX Claim 19; Fig 11; 141pp; English.
 PS
 XX
 CC This sequence represents the Aspergillus ficum phytase sequence. The
 CC invention relates to variant phytase enzymes with specific amino acid
 CC substitutions for improved properties. The phytase variants can be used
 CC for liberating phosphorus from a phytase substrate. They can be used for
 CC reducing phytate levels in animal manure. They can be used in feed or
 CC food preparations. The phytase DNA can also be used to produce transgenic
 CC plants which can be used in feeds or foods. The phytase variants can also
 CC be used in soy processing and in the manufacture of inositol or
 CC derivatives. The phytase variants can have altered activities such as pH
 CC stability, temperature stability, pH profile, temperature profile,
 CC specific activity (in particular in relation to pH and temperature),
 CC substrate specificity, substrate cleavage pattern, substrate binding,
 CC position specificity, the velocity and level of release of phosphate from
 CC corn, reaction rate, phytase degradation rate and end level of released
 CC phosphate reached
 XX
 SQ Sequence 467 AA;
 Query Match 99.8%; Score 2353; DB 2; Length 467;
 Best Local Similarity 100.0%; Pred. No. 1.8e-215;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFPAQVL 61
 DB 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFPAQVL 79
 QY 62 SRHGARYPTDSKGKYSALIEEIQONATTFDGKVAFLKTYNYSIGADDLTPFGQELVNS 121
 DB 80 SRHGARYPTDSKGKYSALIEEIQONATTFDGKVAFLKTYNYSIGADDLTPFGQELVNS 139
 QY 122 GIKFYQRYESLTRNIVPPIRSGSSRVIASGKFFIEGFQSTKLKDPRAQPGQSSPKIDVV 181
 DB 140 GIKFYQRYESLTRNIVPPIRSGSSRVIASGKFFIEGFQSTKLKDPRAQPGQSSPKIDVV 199
 QY 182 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDSGLVTLTDTVTY 241
 DB 200 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDSGLVTLTDTVTY 259
 QY 242 LMDMCSFDTISTSTVDTKLSFCDLFTHDEWINDYQLSKKYYGHGAGNPLGPTQGVGY 301
 DB 260 LMDMCSFDTISTSTVDTKLSFCDLFTHDEWINDYQLSKKYYGHGAGNPLGPTQGVGY 319
 QY 302 ANELIARLTHSPVHDDTSSNHTLSSPATPLNLTLYADFSDHNGIISILFALGLYNGTK 361
 DB 320 ANELIARLTHSPVHDDTSSNHTLSSPATPLNLTLYADFSDHNGIISILFALGLYNGTK 379
 QY 362 PLSTTTVENTITQDGFSSANTVPASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 421
 DB 380 PLSTTTVENTITQDGFSSANTVPASRLYVEMMQCAEQEPLVRVLVNDRVVPLHGCPVD 439
 QY 422 ALGRCRDSFVRGLSFARSGGDWAECEFA 449
 DB 440 ALGRCRDSFVRGLSFARSGGDWAECEFA 467

RESULT 7
 ABB83810
 ID ABB83810 standard; protein; 467 AA.
 XX
 AC ABB83810;
 XX
 DT 17-SEP-2002 (first entry)
 XX
 DE Aspergillus niger phyA related polypeptide 1.
 XX
 KW Yeast; Aspergillus niger; phytase; phyA; Pasteur Pichia; enzyme.
 XX
 OS Aspergillus niger.
 XX
 PN CN1333363-A.
 XX
 XX 30-JAN-2002.
 XX
 XX 12-JUL-2000; 2000CN-00117245.
 XX
 XX 12-JUL-2000; 2000CN-00117245.
 XX
 XX (RAIS-) INST RAISE LIVESTOCK GUANGDONG ACAD AGRI.
 XX
 XX Chen Z, Yang L, Fang L;
 XX
 XX WPI; 2002-305615/35.
 DR N-PSDB; ABN85588.
 XX
 XX Phytase gene sequence and application in yeast thereof.
 PT
 XX Disclosure; Fig 2; 48pp; Chinese.
 PS
 XX
 CC The invention relates to a coded phytase gene sequence suitable for
 CC secretion and expression in yeast and its application. It is mainly
 CC characterised by removing nucleotide sequence of +45-+146 bit from phyA
 CC total length structure gene sequence, removing Aspergillus niger signal
 CC peptide coded sequence of +1-+44 and +147-+159, connecting a part of
 CC signal peptide code sequence suitable for secretion and expression at 5',
 CC end and connecting a restriction endonuclease site at 3' end. The
 CC different carriers can be connected into said gene sequence so as to form
 CC a recombinant plasmid with different functions and after the recombinant
 CC plasmid using pPICZ alpha A as carrier is converted into Pasteur Pichia
 CC yeast, finally the invented Pasteur Pichia yeast engineering bacterium
 CC (CCTCC NO:RM200005) can be obtained through the screening process. By
 CC using the invention the industrial process of phytase bio-expression can
 CC be successfully implemented. The present sequence is that of a
 CC polypeptide of the invention
 XX
 SQ Sequence 467 AA;
 Query Match 99.8%; Score 2353; DB 5; Length 467;
 Best Local Similarity 100.0%; Pred. No. 1.8e-215;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFPAQVL 61
 DB 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFPAQVL 79
 QY 62 SRHGARYPTDSKGKYSALIEEIQONATTFDGKVAFLKTYNYSIGADDLTPFGQELVNS 121
 DB 80 SRHGARYPTDSKGKYSALIEEIQONATTFDGKVAFLKTYNYSIGADDLTPFGQELVNS 139
 QY 122 GIKFYQRYESLTRNIVPPIRSGSSRVIASGKFFIEGFQSTKLKDPRAQPGQSSPKIDVV 181
 DB 140 GIKFYQRYESLTRNIVPPIRSGSSRVIASGKFFIEGFQSTKLKDPRAQPGQSSPKIDVV 199
 QY 182 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDSGLVTLTDTVTY 241
 DB 200 ISEASSNNLTDPGCTCTVFEDSELADTVEANFTATFVPSIRQRLNDSGLVTLTDTVTY 259
 QY 242 LMDMCSFDTISTSTVDTKLSFCDLFTHDEWINDYQLSKKYYGHGAGNPLGPTQGVGY 301

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Db 260 LMDMCSFDTISTSTVDTKLSPFCDLFTDHEWNYDYLQSLKKYHGHGAGNPLGPTQGVY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGHIIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGHIIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQDGFSSAWTPPFASRLYVEMWQCAEQEPLVRLVNDRVVPLHGCPCVD 421
Db 380 PLSTTTVENITQDGFSSAWTPPFASRLYVEMWQCAEQEPLVRLVNDRVVPLHGCPCVD 439
QY 422 ALGRCTRDSFVRGLSFARSGDWAECA 449
Db 440 ALGRCTRDSFVRGLSFARSGDWAECA 467

RESULT 8
ADL91242
ID ADL91242 standard; protein; 467 AA.

XX AC ADL91242;
XX 17-JUN-2004 (first entry)
XX DE Wild-type phytase, SEQ ID 2.
XX KW Phytase; enzyme; foodstuff; animal feed; inositol phosphate.

XX OS Aspergillus niger.
XX PN WC2004024885-A2.
XX PD 25-MAR-2004.
XX PF 15-SEP-2003; 2003WO-US028923.
XX PR 13-SEP-2002; 2002US-0410736P.
XX PA (CORR) CORNELL RES FOUND INC.
XX PA (USDA) US SEC OF AGRIC.
XX PI Lei X, Mullaney EJ, Ullah AHJ;
XX XX WPI; 2004-270029/25.
XX DR N-PSDB; ADL91241.

XX Novel isolated mutant phytase e.g. PhyA useful for feeding monogastric
XX animals, improving nutritional value of foodstuffs consumed by animal, in
XX vitro hydrolysis of phytate or improving nutritional value of foodstuffs
XX consumed by humans.

XX Example 1; SEQ ID NO 2; 215pp; English.

XX The present invention relates to mutant phytases (I) and their coding
XX sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
XX (I) have altered pH profiles and altered pH optima compared to a
XX corresponding non-mutant phytase. (I) are useful for improving the
XX nutritional value of a foodstuff which involves providing a foodstuff
XX comprising myo-inositol hexakisphosphate, providing (I) and feeding to
XX the animal the foodstuff in combination with (I) under conditions
XX effective to increase the bioavailability of phosphate from phytate. (I)
XX are also useful for feeding a monogastric animal (e.g., fowl species,
XX porcine species, aquatic species, domestic animal chosen from canine
XX species and a feline species, or mammalian species chosen from
XX Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
XX foodstuff in combination with (I), to the animal. (I) are also useful for
XX producing specific inositol phosphate metabolites or products for
XX nutritional and biomedical applications. The present sequence is a wild-
XX type phytase, which was used to produce the mutants of the invention.

XX Sequence 467 AA;

XX Query Match 99.8%; Score 2353; DB 8; Length 467;

Best Local Similarity 100.0%; Pred. No. 1.8e-215; Indels 0; Gaps 0;
Matches 448; Conservative 0; Mismatches 0;
QY 2 LAVPASRNCSCDVTVDQGYQCFSETHLWGVAPFPFSLANESVISPVEPAGCRVTFQAQVL 61
Db 20 LAVPASRNCSCDVTVDQGYQCFSETHLWGVAPFPFSLANESVISPVEPAGCRVTFQAQVL 79
QY 62 SRHGARYPTDSKGKYSALIEEIQONATTFDGKYAFLLKTYNYSLSGADDLTPFGEQELVNS 121
Db 80 SRHGARYPTDSKGKYSALIEEIQONATTFDGKYAFLLKTYNYSLSGADDLTPFGEQELVNS 139
QY 122 GIKFYQRYESLTRNIVPFISSGSSRVIASGKKFIEGQSTKLKDPRAQPGOSSPKIDVV 181
Db 140 GIKFYQRYESLTRNIVPFISSGSSRVIASGKKFIEGQSTKLKDPRAQPGOSSPKIDVV 199
QY 182 ISEASSNNLTDPGCTVFEDSELADTVEANFTAFVPSIRORLENDLSGVTLTDEVTY 241
Db 200 ISEASSNNLTDPGCTVFEDSELADTVEANFTAFVPSIRORLENDLSGVTLTDEVTY 259
QY 242 LMDMCSFDTISTSTVDTKLSPFCDLFTDHEWNYDYLQSLKKYHGHGAGNPLGPTQGVY 301
Db 260 LMDMCSFDTISTSTVDTKLSPFCDLFTDHEWNYDYLQSLKKYHGHGAGNPLGPTQGVY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGHIIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGHIIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQDGFSSAWTPPFASRLYVEMWQCAEQEPLVRLVNDRVVPLHGCPCVD 421
Db 380 PLSTTTVENITQDGFSSAWTPPFASRLYVEMWQCAEQEPLVRLVNDRVVPLHGCPCVD 439
QY 422 ALGRCTRDSFVRGLSFARSGDWAECA 449
Db 440 ALGRCTRDSFVRGLSFARSGDWAECA 467

RESULT 9
ADL91268
ID ADL91268 standard; protein; 467 AA.

XX AC ADL91268;
XX 17-JUN-2004 (first entry)
XX DE Mutant phytase, K300R, SEQ ID 28.
XX KW Mutant; mutant; phytase; enzyme; foodstuff; animal feed;
XX KW inositol phosphate.
XX OS Aspergillus niger.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 300 /note= "Wild-type residue replaced with Arg"
XX PN WO2004024885-A2.
XX PD 25-MAR-2004.
XX PF 15-SEP-2003; 2003WO-US028923.
XX PR 13-SEP-2002; 2002US-0410736P.
XX PA (CORR) CORNELL RES FOUND INC.
XX PA (USDA) US SEC OF AGRIC.
XX PI Lei X, Mullaney EJ, Ullah AHJ;
XX XX WPI; 2004-270029/25.
XX DR N-PSDB; ADL91267.
XX Novel isolated mutant phytase e.g. PhyA useful for feeding monogastric

PT animals, improving nutritional value of foodstuffs consumed by animal, in
 PT vitro hydrolysis of phytate or improving nutritional value of foodstuffs
 consumed by humans.

XX PS Claim 40; SEQ ID NO 28; 215pp; English.

XX The present invention relates to mutant phytases (I) and their coding
 CC sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
 CC (I) have altered pH profiles and altered pH optima compared to a
 CC corresponding non-mutant phytase. (I) are useful for improving the
 CC nutritional value of a foodstuff which involves providing a foodstuff
 CC comprising myo-inositol hexakisphosphate, providing (I) and feeding to
 CC the animal the foodstuff in combination with (I) under conditions
 CC effective to increase the bioavailability of phosphate from phytate. (I)
 CC are also useful for feeding a monogastric animal (e.g., fowl species,
 CC porcine species, aquatic species, domestic animal chosen from canine
 CC species and a feline species, or mammalian species chosen from
 CC Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
 CC foodstuff in combination with (I), to the animal. (I) are also useful for
 CC producing specific inositol phosphate metabolites or products for
 CC nutritional and biomedical applications. The present sequence is one such
 CC mutant phytase.

XX SQ Sequence 467 AA;

Query Match 99.7%; Score 2350; DB 8; Length 467;

Best Local Similarity 99.8%; Pred. No. 3.5e-215;
 Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQGYQCFSESHLWGQYAPFSLANESVISEVPAGCRVTFQAQVL 61
 Db 20 LAVPASRNQSSCDTVDQGYQCFSESHLWGQYAPFSLANESVISEVPAGCRVTFQAQVL 79
 QY 62 SRHGARYPTDSKGYKYSALIEIQONATTFDGKAFKTYNSLGGADLTTPFGEQELVNS 121
 Db 80 SRHGARYPTDSKGYKYSALIEIQONATTFDGKAFKTYNSLGGADLTTPFGEQELVNS 139
 QY 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKFFIEGFQSTKLDPRAQPGQSSPKIDVV 181
 Db 140 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKFFIEGFQSTKLDPRAQPGQSSPKIDVV 199
 QY 182 ISEASSNNLTDPGCTVFEDESEADTVEANFTATFVPSIRQLENLSGVTLTDEVTV 241
 Db 200 ISEASSNNLTDPGCTVFEDESEADTVEANFTATFVPSIRQLENLSGVTLTDEVTV 259
 QY 242 LMDMCSFTTISTSTVDTKLSPFCDLFTHDEWINYDLSLKYKHGAGNPLGPTQGVGY 301
 Db 260 LMDMCSFTTISTSTVDTKLSPFCDLFTHDEWINYDLSLKYKHGAGNPLGPTQGVGY 319
 QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 361
 Db 320 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 379
 QY 362 PLSTTTVNITQTDFSSAWTVPPASRLYVEMMQCAEQEPLRVLRVNDVRVPLHGCPVD 421
 Db 380 PLSTTTVNITQTDFSSAWTVPPASRLYVEMMQCAEQEPLRVLRVNDVRVPLHGCPVD 439
 QY 422 ALGRCTRDSFVRGLSFARSGGDWAECEFA 449
 Db 440 ALGRCTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 10

ADL91262

ID ADL91262 standard; protein; 467 AA.

XX AC ADL91262;

XX 17-JUN-2004 (first entry)

DT Mutant phytase, E228Q, SEQ ID 22.

DE Mutant; mutein; phytase; enzyme; foodstuff; animal feed;

XX

KW

KW inositol phosphate.
 XX Aspergillus niger.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 228 /note= "Wild-type residue replaced with Gln"

XX WO2004024885-A2.

XX 25-MAR-2004.

XX 15-SEP-2003; 2003WO-US028923.

XX 13-SEP-2002; 2002US-0410736P.

XX (CORR) CORNELL RES FOUND INC.

XX (USDA) US SEC OF AGRIC.

XX Lei X, Mullaney EJ, Ullah AHJ;

XX WPI; 2004-270029/25.

XX N-PSDB; ADL91261.

XX Novel isolated mutant phytase e.g. PhytA useful for feeding monogastric
 PT animals, improving nutritional value of foodstuffs consumed by animal, in
 PT vitro hydrolysis of phytate or improving nutritional value of foodstuffs
 consumed by humans.

XX Claim 38; SEQ ID NO 22; 215pp; English.

XX The present invention relates to mutant phytases (I) and their coding
 CC sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
 CC (I) have altered pH profiles and altered pH optima compared to a
 CC corresponding non-mutant phytase. (I) are useful for improving the
 CC nutritional value of a foodstuff which involves providing a foodstuff
 CC comprising myo-inositol hexakisphosphate, providing (I) and feeding to
 CC the animal the foodstuff in combination with (I) under conditions
 CC effective to increase the bioavailability of phosphate from phytate. (I)
 CC are also useful for feeding a monogastric animal (e.g., fowl species,
 CC porcine species, aquatic species, domestic animal chosen from canine
 CC species and a feline species, or mammalian species chosen from
 CC Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
 CC foodstuff in combination with (I), to the animal. (I) are also useful for
 CC producing specific inositol phosphate metabolites or products for
 CC nutritional and biomedical applications. The present sequence is one such
 CC mutant phytase.

XX SQ Sequence 467 AA;

Query Match 99.7%; Score 2350; DB 8; Length 467;

Best Local Similarity 99.8%; Pred. No. 3.5e-215;
 Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQGYQCFSESHLWGQYAPFSLANESVISEVPAGCRVTFQAQVL 61
 Db 20 LAVPASRNQSSCDTVDQGYQCFSESHLWGQYAPFSLANESVISEVPAGCRVTFQAQVL 79
 QY 62 SRHGARYPTDSKGYKYSALIEIQONATTFDGKAFKTYNSLGGADLTTPFGEQELVNS 121
 Db 80 SRHGARYPTDSKGYKYSALIEIQONATTFDGKAFKTYNSLGGADLTTPFGEQELVNS 139
 QY 122 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKFFIEGFQSTKLDPRAQPGQSSPKIDVV 181
 Db 140 GIKFYQRYESLTRNIVPFIRSSGSSRVIASGKFFIEGFQSTKLDPRAQPGQSSPKIDVV 199
 QY 182 ISEASSNNLTDPGCTVFEDESEADTVEANFTATFVPSIRQLENLSGVTLTDEVTV 241
 Db 200 ISEASSNNLTDPGCTVFEDESEADTVEANFTATFVPSIRQLENLSGVTLTDEVTV 259
 QY 242 LMDMCSFTTISTSTVDTKLSPFCDLFTHDEWINYDLSLKYKHGAGNPLGPTQGVGY 301
 Db 260 LMDMCSFTTISTSTVDTKLSPFCDLFTHDEWINYDLSLKYKHGAGNPLGPTQGVGY 319
 QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 361
 Db 320 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSDHNGIISILFALGLYNGTK 379
 QY 362 PLSTTTVNITQTDFSSAWTVPPASRLYVEMMQCAEQEPLRVLRVNDVRVPLHGCPVD 421
 Db 380 PLSTTTVNITQTDFSSAWTVPPASRLYVEMMQCAEQEPLRVLRVNDVRVPLHGCPVD 439
 QY 422 ALGRCTRDSFVRGLSFARSGGDWAECEFA 449
 Db 440 ALGRCTRDSFVRGLSFARSGGDWAECEFA 467

Db	260	LMDMCSFTISTSTVDYTKLSPPCDLFTDHEWINDYQLSKKYYGHGAGNPLGPTQGVGY	319
Qy	302	ANELIARLTHSPVHDDTSSNHTLSDSPATFPPLNSTLYADFSDNGLIISILFALGLYNGTK	361
Db	320	ANELIARLTHSPVHDDTSSNHTLSDSPATFPPLNSTLYADFSDNGLIISILFALGLYNGTK	379
Qy	362	PLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCAOEPLVRVLVNDRVVPLHGCPVD	421
Db	380	PLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCAOEPLVRVLVNDRVVPLHGCPVD	439
Qy	422	ALGCRTRDSFVRGLSPARSGDWAECFA	449
Db	440	ALGCRTRDSFVRGLSPARSGDWAECFA	467
RESULT 11			
ID	ADL91260		
XX	ADL91260 standard; protein; 467 AA.		
AC	ADL91260;		
XX			
DT	17-JUN-2004 (first entry)		
XX			
DE	Mutant phytase, K94E, SEQ ID 20.		
XX			
KW	Mutant; mutein; phytase; enzyme; foodstuff; animal feed;		
KW	inositol phosphate.		
XX			
OS	Aspergillus niger.		
OS	Synthetic.		
XX			
XX	Key	Location/Qualifiers	
PH	Misc-difference 94		
FT	/note= "Wild-type residue replaced with Glu"		
XX			
XX	WO2004024885-A2.		
XX			
PD	25-MAR-2004.		
XX			
PF	15-SEP-2003; 2003WO-US028923.		
XX			
PR	13-SEP-2002; 2002US-0410736P.		
XX			
XX	(CORR) CORNELL RES FOUND INC.		
PA	(USDA) US SEC OF AGRIC.		
XX			
PI	Lei X, Mullaney EJ, Ullah AHJ;		
XX			
DR	WPI; 2004-270029/25.		
XX	N-FSDB; ADL91259.		
XX			
XX	Novel isolated mutant phytase e.g. PhyA useful for feeding monogastric		
PT	animals, improving nutritional value of foodstuffs consumed by animal, in		
PT	vitro hydrolysis of phytate or improving nutritional value of foodstuffs		
PT	consumed by humans.		
XX			
FS	Claim 37; SEQ ID NO 20; 215pp; English.		
XX			
CC	The present invention relates to mutant phytases (I) and their coding		
CC	sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).		
CC	(I) have altered pH profiles and altered pH optima compared to a		
CC	corresponding non-mutant phytase. (I) are useful for improving the		
CC	nutritional value of a foodstuff, which involves providing a foodstuff		
CC	comprising myo-inositol hexakisphosphate, providing (I) and feeding to		
CC	the animal the foodstuff in combination with (I) under conditions		
CC	effective to increase the bioavailability of phosphate from phytate. (I)		
CC	are also useful for feeding a monogastric animal (e.g., fowl species,		
CC	porcine species, aquatic species, domestic animal chosen from		
CC	species and a feline species, or mammalian species chosen from		
CC	Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding		
CC	foodstuff in combination with (I), to the animal. (I) are also useful for		
CC	producing specific inositol phosphate metabolites or products for		
CC	nutritional and biomedical applications. The present sequence is one such		

CC	mutant phytase.		
XX			
SQ	Sequence 467 AA;		
Query Match			
Best Local Similarity 99.6%; Score 2349; DB 8; Length 467;			
Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Qy	2	LAVPASRQSSCDTVDQGYQCFSETSHLWGQVAPFPFSLANESVISPVEVAGCRVTPFAQVL	61
Db	20	LAVPASRQSSCDTVDQGYQCFSETSHLWGQVAPFPFSLANESVISPVEVAGCRVTPFAQVL	79
Qy	62	SRHGARYPTDSKGYKYSALIEIQNATTFDCKYAFKTYNSLGGADDLTPFGEQELVNS	121
Db	80	SRHGARYPTDSKGYKYSALIEIQNATTFDCKYAFKTYNSLGGADDLTPFGEQELVNS	139
Qy	122	GKIFYORYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVV	181
Db	140	GKIFYORYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVV	199
Qy	182	ISEASSNNLTDPGCTCTVFEDSELADTVANFTATVPFPIRQLENDLSGVTITDTEVTY	241
Db	200	ISEASSNNLTDPGCTCTVFEDSELADTVANFTATVPFPIRQLENDLSGVTITDTEVTY	259
Qy	242	LMDMCSFDTISTSTVDYTKLSPPCDLFTDHEWINDYQLSKKYYGHGAGNPLGPTQGVGY	301
Db	260	LMDMCSFDTISTSTVDYTKLSPPCDLFTDHEWINDYQLSKKYYGHGAGNPLGPTQGVGY	319
Qy	302	ANELIARLTHSPVHDDTSSNHTLSDSPATFPPLNSTLYADFSDNGLIISILFALGLYNGTK	361
Db	320	ANELIARLTHSPVHDDTSSNHTLSDSPATFPPLNSTLYADFSDNGLIISILFALGLYNGTK	379
Qy	362	PLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCAOEPLVRVLVNDRVVPLHGCPVD	421
Db	380	PLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCAOEPLVRVLVNDRVVPLHGCPVD	439
Qy	422	ALGCRTRDSFVRGLSPARSGDWAECFA	449
Db	440	ALGCRTRDSFVRGLSPARSGDWAECFA	467
RESULT 12			
ID	ADL91264	ADL91264 standard; protein; 467 AA.	
XX	ADL91264;		
XX			
DT	17-JUN-2004 (first entry)		
XX			
DE	Mutant phytase, E228K, SEQ ID 24.		
XX			
KW	Mutant; mutein; phytase; enzyme; foodstuff; animal feed;		
KW	inositol phosphate.		
XX			
OS	Aspergillus niger.		
OS	Synthetic.		
XX			
PH	Key	Location/Qualifiers	
FT	Misc-difference 228		
FT	/note= "Wild-type residue replaced with Lys"		
XX			
XX	WO2004024885-A2.		
XX			
PD	25-MAR-2004.		
XX			
PF	15-SEP-2003; 2003WO-US028923.		
XX			
PR	13-SEP-2002; 2002US-0410736P.		
XX			
XX	(CORR) CORNELL RES FOUND INC.		
PA	(USDA) US SEC OF AGRIC.		
XX			
PI	Lei X, Mullaney EJ, Ullah AHJ;		
XX			

XX WPI; 2004-270029/25.
DR N-PSDB; ADL91263.
XX
PT Novel isolated mutant phytase e.g. PhyA useful for feeding monogastric
KW animals, improving nutritional value of foodstuffs consumed by animal, in
PT vitro hydrolysis of phytate or improving nutritional value of foodstuffs
XX consumed by humans.
PS
XX Claim 38; SEQ ID NO 24; 215pp; English.
XX
CC The present invention relates to mutant phytases (I) and their coding
CC sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
CC (I) have altered pH profiles and altered pH optima compared to a
CC corresponding non-mutant phytase. (I) are useful for improving the
CC nutritional value of a foodstuff which involves providing a foodstuff
CC comprising myo-inositol hexakisphosphate, providing (I) and feedings to
CC the animal the foodstuff in combination with (I) under conditions
CC effective to increase the bioavailability of phosphate from phytate. (I)
CC are also useful for feeding a monogastric animal (e.g., fowl species,
CC porcine species, aquatic species, domestic animal chosen from canine
CC species and a feline species, or mammalian species chosen from
CC Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
CC foodstuff in combination with (I), to the animal. (I) are also useful for
CC producing specific inositol phosphate metabolites or products for
CC nutritional and biomedical applications. The present sequence is one such
CC mutant phytase.
XX
XX
SQ Sequence 467 AA;
Query Match 99.6%; Score 2349; DB 8; Length 467;
Best Local Similarity 99.8%; Pred. No. 4.4e-215;
Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 LAVPASRNSQSCDVTVDGQYQCFSTSHLWGOYAPFFSLANESVISPVPAGCRVTFPAQVL 61
DB 20 LAVPASRNSQSCDVTVDGQYQCFSTSHLWGOYAPFFSLANESVISPVPAGCRVTFPAQVL 79
QY 62 SRHGARYPTDSKGKYSALIEEQONATTFDGKYAFKTYNYSIGADDLTPFGQELVNS 121
DB 80 SRHGARYPTDSKGKYSALIEEQONATTFDGKYAFKTYNYSIGADDLTPFGQELVNS 139
QY 122 GIKFYQRYESLTRNIVPFISSGSSSRVSIASGKFFIEGFQSTKLDPRAQPGQSSPKIDVV 181
DB 140 GIKFYQRYESLTRNIVPFISSGSSSRVSIASGKFFIEGFQSTKLDPRAQPGQSSPKIDVV 199
QY 182 ISEASSNNLDPGTCVTFEDSELADTVKANFTTFVPSIRQRLNDSGVTLTDTVTY 241
DB 200 ISEASSNNLDPGTCVTFEDSELADTVKANFTTFVPSIRQRLNDSGVTLTDTVTY 259
QY 242 LMDMCSFDTTSTVDTKLSPFCDLFTHDEWINDYQLSKLKYGHGAGNPLGPTQGVY 301
DB 260 LMDMCSFDTTSTVDTKLSPFCDLFTHDEWINDYQLSKLKYGHGAGNPLGPTQGVY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATFPINSTLYADFSDHNGIISILFALGLYNGTK 361
DB 320 ANELIARLTHSPVHDDTSSNHTLDSPPATFPINSTLYADFSDHNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENTITQDGFSAWTVPPASRLYVEMMOCQAEQBLVRLVNDVRVPLHGCPVD 421
DB 380 PLSTTTVENTITQDGFSAWTVPPASRLYVEMMOCQAEQBLVRLVNDVRVPLHGCPVD 439
QY 422 ALGRCTRDSFVRGLSFARSGGDWAECEA 449
DB 440 ALGRCTRDSFVRGLSFARSGGDWAECEA 467
RESULT 13
ADL91274
ID ADL91274 standard; protein; 467 AA.
XX
AC ADL91274;
XX

DT 17-JUN-2004 (first entry)
XX
XX Mutant phytase, K301E, SEQ ID 34.
DE
XX
XX Mutant; mutein; phytase; enzyme; foodstuff; animal feed;
KW inositol phosphate.
XX
XX Aspergillus niger.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 301
FT /note= "Wild-type residue replaced with Glu"
FT
FN WO2004024885-A2.
XX
XX 25-MAR-2004.
PD
XX 15-SEP-2003; 2003WO-US028923.
FF
XX 13-SEP-2002; 2002US-0410736P.
PR
XX (CORR) CORNELL RES FOUND INC.
FA (USDA) US SEC OF AGRIC.
PA
XX Lei X, Mullaney EJ, Ullah AHJ;
PI
XX WPI; 2004-270029/25.
DR N-PSDB; ADL91273.
DR
XX
XX Novel isolated mutant phytase e.g. PhyA useful for feeding monogastric
PT animals, improving nutritional value of foodstuffs consumed by animal, in
PT vitro hydrolysis of phytate or improving nutritional value of foodstuffs
PT consumed by humans.
XX
XX Claim 41; SEQ ID NO 34; 215pp; English.
PS
XX
CC The present invention relates to mutant phytases (I) and their coding
CC sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
CC (I) have altered pH profiles and altered pH optima compared to a
CC corresponding non-mutant phytase. (I) are useful for improving the
CC nutritional value of a foodstuff which involves providing a foodstuff
CC comprising myo-inositol hexakisphosphate, providing (I) and feedings to
CC the animal the foodstuff in combination with (I) under conditions
CC effective to increase the bioavailability of phosphate from phytate. (I)
CC are also useful for feeding a monogastric animal (e.g., fowl species,
CC porcine species, aquatic species, domestic animal chosen from canine
CC species and a feline species, or mammalian species chosen from
CC Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
CC foodstuff in combination with (I), to the animal. (I) are also useful for
CC producing specific inositol phosphate metabolites or products for
CC nutritional and biomedical applications. The present sequence is one such
CC mutant phytase.
XX
XX
SQ Sequence 467 AA;
Query Match 99.6%; Score 2349; DB 8; Length 467;
Best Local Similarity 99.8%; Pred. No. 4.4e-215;
Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 LAVPASRNSQSCDVTVDGQYQCFSTSHLWGOYAPFFSLANESVISPVPAGCRVTFPAQVL 61
DB 20 LAVPASRNSQSCDVTVDGQYQCFSTSHLWGOYAPFFSLANESVISPVPAGCRVTFPAQVL 79
QY 62 SRHGARYPTDSKGKYSALIEEQONATTFDGKYAFKTYNYSIGADDLTPFGQELVNS 121
DB 80 SRHGARYPTDSKGKYSALIEEQONATTFDGKYAFKTYNYSIGADDLTPFGQELVNS 139
QY 122 GIKFYQRYESLTRNIVPFISSGSSSRVSIASGKFFIEGFQSTKLDPRAQPGQSSPKIDVV 181
DB 140 GIKFYQRYESLTRNIVPFISSGSSSRVSIASGKFFIEGFQSTKLDPRAQPGQSSPKIDVV 199
QY 182 ISEASSNNLDPGTCVTFEDSELADTVKANFTTFVPSIRQRLNDSGVTLTDTVTY 241

||||| 200 ISEASSNNLTDPGCTVFEDSELADTVEANFTATVPISIRQRLNDLSGVTLTDEVTY 259
QY 242 LMDMCSFDITSTVDTKLSPPCDLFTHDEWNYDLSKYYKGAGNPLGPTQGVY 301
Db 260 LMDMCSFDITSTVDTKLSPPCDLFTHDEWNYDLSKYYKGAGNPLGPTQGVY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQDGFSSAWTVFFASRLYVENMQCAEQEPLVRLVNDVRVPLHGCPVD 421
Db 380 PLSTTTVENITQDGFSSAWTVFFASRLYVENMQCAEQEPLVRLVNDVRVPLHGCPVD 439
QY 422 ALGRCTRDSFVRGLSFARSGGDWAECA 449
Db 440 ALGRCTRDSFVRGLSFARSGGDWAECA 467

RESULT 14
ADL91248
ID ADL91248 standard; protein; 467 AA.
AC ADL91248;
XX
DT 17-JUN-2004 (first entry)
XX
DE Mutant phytase, K300E, SEQ ID 8.
XX
KW Mutant; mutein; phytase; enzyme; foodstuff; animal feed;
KW inositol phosphate.
XX
OS Aspergillus niger.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 300 /note= "wild-type residue replaced with Glu"
FT
XX
PN WO2004024885-A2.
XX
PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US028923.
XX
PR 13-SEP-2002; 2002US-0410736P.
XX
PA (CORR) CORNELL RES FOUND INC.
PA (USDA) US SEC OF AGRIC.
XX
PI Lei X, Mullaney BJ, Ullah AHJ;
XX
DR WPI; 2004-270029/25.
DR N-PSDB; ADL91247.
XX
XX Novel isolated mutant phytase e.g. Phya useful for feeding monogastric
PT animals, improving nutritional value of foodstuffs consumed by animal, in
PT vitro hydrolysis of phytate or improving nutritional value of foodstuffs
PT consumed by humans.
XX
PS Claim 40; SEQ ID NO 8; 215pp; English.
XX
XX The present invention relates to mutant phytases (I) and their coding
CC sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
CC (I) have altered pH profiles and altered pH optima compared to a
CC corresponding non-mutant phytase. (I) are useful for improving the
CC nutritional value of a foodstuff which involves providing a foodstuff
CC comprising myo-inositol hexakisphosphate, providing (I) and feeding to
CC the animal the foodstuff in combination with (I) under conditions
CC effective to increase the bioavailability of phosphate from phytate. (I)
CC are also useful for feeding a monogastric animal (e.g., fowl species,
XX porcine species, aquatic species, domestic animal chosen from canine

CC species and a feline species, or mammalian species chosen from
CC Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
CC foodstuff in combination with (I), to the animal. (I) are also useful for
CC producing specific inositol phosphate metabolites or products for
CC nutritional and biomedical applications. The present sequence is one such
CC mutant phytase.
XX
SQ Sequence 467 AA;
Query Match 99.6%; Score 2349; DB 8; Length 467;
Best Local Similarity 99.8%; Pred. No. 4.4e-215;
Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQVAPFFSLANESVISPEVPAGCRVTFPAQVL 61
Db 20 LAVPASRNQSSCDTVDQGYQCFSETSHLWGQVAPFFSLANESVISPEVPAGCRVTFPAQVL 79
QY 62 SRHGARYPTDSKGKYSALIEIQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNS 121
Db 80 SRHGARYPTDSKGKYSALIEIQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNS 139
QY 122 GIKFYQRYESLTRNIVPFRSSGSRVIAASGKKFIEGFQSTKLKDPRAQPGSSPKIDV 181
Db 140 GIKFYQRYESLTRNIVPFRSSGSRVIAASGKKFIEGFQSTKLKDPRAQPGSSPKIDV 199
QY 182 ISEASSNNLTDPGCTVFEDSELADTVEANFTATVPISIRQRLNDLSGVTLTDEVTY 241
Db 200 ISEASSNNLTDPGCTVFEDSELADTVEANFTATVPISIRQRLNDLSGVTLTDEVTY 259
QY 242 LMDMCSFDITSTVDTKLSPPCDLFTHDEWNYDLSKYYKGAGNPLGPTQGVY 301
Db 260 LMDMCSFDITSTVDTKLSPPCDLFTHDEWNYDLSKYYKGAGNPLGPTQGVY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db 320 ANELIARLTHSPVHDDTSSNHTLDSPPATFPLNSTLYADFSHDNGIISILFALGLYNGTK 379
QY 362 PLSTTTVENITQDGFSSAWTVFFASRLYVENMQCAEQEPLVRLVNDVRVPLHGCPVD 421
Db 380 PLSTTTVENITQDGFSSAWTVFFASRLYVENMQCAEQEPLVRLVNDVRVPLHGCPVD 439
QY 422 ALGRCTRDSFVRGLSFARSGGDWAECA 449
Db 440 ALGRCTRDSFVRGLSFARSGGDWAECA 467

RESULT 15
ADL91258
ID ADL91258 standard; protein; 467 AA.
XX
AC ADL91258;
XX
DT 17-JUN-2004 (first entry)
XX
DE Mutant phytase, K91E, SEQ ID 18.
XX
KW Mutant; mutein; phytase; enzyme; foodstuff; animal feed;
KW inositol phosphate.
XX
OS Aspergillus niger.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 91 /note= "wild-type residue replaced with Glu"
FT
XX
PN WO2004024885-A2.
XX
PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US028923.
XX
PR 13-SEP-2002; 2002US-0410736P.

Job time : 117 secs

```
XX (CORR ) CORNELL RES FOUND INC.
PA (USDA ) US SEC OF AGRIC.
XX
PI Lei X, Mullaney EJ, Ullah AHJ;
XX
DR WPI; 2004-270029/25.
DR N-PSDB; ADL91257.
XX
PT Novel isolated mutant phytase e.g. Phya useful for feeding monogastric
PT animals, improving nutritional value of foodstuffs consumed by animal, in
PT vitro hydrolysis of phytate or improving nutritional value of foodstuffs
PT consumed by humans.
XX
PS Claim 36; SEQ ID NO 18; 215pp; English.
XX
CC The present invention relates to mutant phytases (I) and their coding
CC sequences (ADL91245-ADL91252, ADL91255-ADL91296, ADL91308 and ADL91309).
CC (I) have altered pH profiles and altered pH optima compared to a
CC corresponding non-mutant phytase. (I) are useful for improving the
CC nutritional value of a foodstuff which involves providing a foodstuff
CC comprising myo-inositol hexakisphosphate, providing (I) and feeding to
CC the animal the foodstuff in combination with (I) under conditions
CC effective to increase the bioavailability of phosphate from phytate. (I)
CC are also useful for feeding a monogastric animal (e.g., fowl species,
CC porcine species, aquatic species, domestic animal chosen from canine
CC species and a feline species, or mammalian species chosen from
CC Oryctolagus, Capra, a Bos, Equus and Ovis species) which involves feeding
CC foodstuff in combination with (I), to the animal. (I) are also useful for
CC producing specific inositol phosphate metabolites or products for
CC nutritional and biomedical applications. The present sequence is one such
CC mutant phytase.
XX
SQ Sequence 467 AA;
Query Match 99.6%; Score 2349; DB 8; Length 467;
Best Local Similarity 99.8%; Pred. NO. 4.4e-215;
Matches 447; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 LAVPASRNQSCDVTDCQYCFSETSHLWQYAPFSLANESVISPEVPAGCRVTFAQVL 61
DB 20 LAVPASRNQSCDVTDCQYCFSETSHLWQYAPFSLANESVISPEVPAGCRVTFAQVL 79
QY 62 SRHGARYPTDSGKKYSALIBEIQONATTFDGKAFKLYNYSLGADDLTPFGQELVNS 121
DB 80 SRHGARYPTDSGKKYSALIBEIQONATTFDGKAFKLYNYSLGADDLTPFGQELVNS 139
QY 122 GIKFYQRYESITRNIVPIRSGSSRVITAGKKFTIEGQSTKLDPRAQPGQSSPKIDV 181
DB 140 GIKFYQRYESITRNIVPIRSGSSRVITAGKKFTIEGQSTKLDPRAQPGQSSPKIDV 199
QY 182 ISEASSNNLDPGCTVFEDSEADTVEANFTATFVPSIRQLENDLSGVTLDTEVTY 241
DB 200 ISEASSNNLDPGCTVFEDSEADTVEANFTATFVPSIRQLENDLSGVTLDTEVTY 259
QY 242 LDMCSEPTISTSTVDTKLSPFCDLFTHEWINVDYLSLKKYKHGAGNPLGPTQGVGY 301
DB 260 LDMCSEPTISTSTVDTKLSPFCDLFTHEWINVDYLSLKKYKHGAGNPLGPTQGVGY 319
QY 302 ANELIARLTHSPVHDDTSSNHTLSSPATFPINSTLYADFSDHNGIITSILFALGLYNGTK 361
DB 320 ANELIARLTHSPVHDDTSSNHTLSSPATFPINSTLYADFSDHNGIITSILFALGLYNGTK 379
QY 362 PLSTTTVENITQTDFSSAWTVPPASRLYVEMMOCQAEQEPPLVRVLVNDVRVPLHGCPVD 421
DB 380 PLSTTTVENITQTDFSSAWTVPPASRLYVEMMOCQAEQEPPLVRVLVNDVRVPLHGCPVD 439
QY 422 ALGRCTRDSFVRGLSFARSGGDWAECEFA 449
DB 440 ALGRCTRDSFVRGLSFARSGGDWAECEFA 467
```

Search completed: October 24, 2004, 12:55:37

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OM protein - protein search, using sw model

Run on: October 24, 2004, 11:16:03 ; Search time 50 Seconds
(without alignments)
864.027 Million cell updates/sec

Title: US-10-089-364-4

Perfect score: 2358

Sequence: 1 MLAVPASRNQSSCDTVDQY.....SFVGLSFARSGDWAECFA 449

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2353	99.8	467	1 JN0656	3-phytase (EC 3.1.1)
2	2315	98.2	441	1 JN0482	3-phytase (EC 3.1.1)
3	2309	97.9	467	1 JN0889	3-phytase (EC 3.1.1)
4	385	16.3	467	1 PABYC	acid phosphatase (
5	385	16.3	467	1 PABYC	acid phosphatase (
6	368	15.6	468	2 S52495	acid phosphatase h
7	352	14.9	467	2 S48996	acid phosphatase (
8	352	14.9	467	2 S53476	acid phosphatase (
9	339.5	14.4	479	1 JN0715	3-phytase (EC 3.1.1)
10	336.5	14.4	479	1 JN0890	acid phosphatase (
11	327	13.9	468	2 J4285	acid phosphatase (
12	300.5	12.7	453	1 A25326	acid phosphatase (
13	300	12.7	463	2 T39929	thiamin-repressibl
14	284	12.0	463	2 S14119	acid phosphatase (
15	148	6.3	468	2 A86233	hypothetical prote
16	132.5	5.6	465	2 JF0369	histidine acid pho
17	120.5	5.1	413	2 F90773	periplasmic glucos
18	120.5	5.1	413	2 B85636	periplasmic glucos
19	119.5	5.1	413	2 JV0087	glucose-1-phosphat
20	119	5.0	449	2 T15933	hypothetical prote
21	115	4.9	590	2 H70130	oligodeopeptidase
22	114.5	4.9	1756	2 A55867	TyB protein - yeas
23	114	4.8	438	2 S46682	acid phosphatase (
24	111.5	4.7	694	2 I40866	exo-alpha-sialidas
25	111.5	4.7	1032	2 T34433	hypothetical prote
26	111	4.7	1816	2 F82901	hypothetical prote
27	109.5	4.6	553	2 T06179	myb-related protei
28	107	4.5	344	2 H83130	protein F52E1.8 [i
29	107	4.5	1322	2 H86196	hypothetical prote

30	107	4.5	2314	1 A46151	protein-tyrosine-p
31	106.5	4.5	1755	2 S45736	TyB protein - yeas
32	106	4.5	507	1 RNZCV	polymerase-associ
33	106	4.5	755	2 T15118	acid phosphatase h
34	106	4.5	3624	2 AD0835	large repetitive p
35	105.5	4.5	411	2 D88504	protein B0361.7 [i
36	105	4.5	380	2 T16883	hypothetical prote
37	105	4.5	452	2 T20556	hypothetical prote
38	104.5	4.4	1254	2 S46636	hypothetical prote
39	104	4.4	504	2 A25222	MSB2 protein - yea
40	104	4.4	1306	2 S25370	threonine synthase
41	103.5	4.4	470	2 D81353	secreted acid phos
42	103	4.4	537	2 S54770	secreted acid phos
43	103	4.4	888	2 T46726	secreted acid phos
44	102	4.3	927	2 T38127	phosphoprotein - f
45	102	4.3	948	2 T11678	hypothetical prote

ALIGNMENTS

RESULT 1

JN0656

3-phytase (EC 3.1.3.8) A precursor - Aspergillus niger

N:Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phyA protein

C:Species: Aspergillus niger

C>Date: 03-Feb-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C:Accession: JN0656; S28456

R:van Hartingsveldt, W.; van Zeijl, C.M.J.; Harteveld, G.M.; Gouka, R.J.; Suykerbuyk, M.F. A.M.J.J.

Gene 127, 87-94, 1993

A:Title: Cloning, characterization and overexpression of the phytase-encoding gene (phyA)

A:Reference number: JN0656; MUID:93252284; PMID:8387447

A:Accession: JN0656

A:Molecule type: DNA

A:Residues: 1-467 <V>

A:Cross-references: UNIPROT:P34752; GB:Z16414; NID:g2392; PIDN:CAA78904.1; PID:g2393

A:Experimental source: strain NRRL3135

A:Note: parts of the sequence, including the amino end of the mature protein, were confir
C:Comment: This enzyme catalyzes the hydrolysis of phytic acid into myo-inositol and inos

C:Genetics:

A:Gene: phyA

A:Introns: 15/2

C:Superfamily: yeast acid phosphatase

C:Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-467/Product: 3-phytase A #status experimental <MAT>

F:27,59,105,120,207,230,339,352,376,389/Binding site: carbohydrate (Asn) (covalent) #stat

F:81,361/Active site: Arg, His #status predicted

F:82/Active site: His (phosphohistidine intermediate) #status predicted

Query Match 99.8%; Score 2353; DB 1; Length 467;

Best Local Similarity 100.0%; Pred. No. 6.2e-164;

Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAVPASRNQSSCDTVDQYQCFSETHLWQYAPFFSLANESVLSPEVPACGRVTFQVL 61

Db LAVPASRNQSSCDTVDQYQCFSETHLWQYAPFFSLANESVLSPEVPACGRVTFQVL 79

QY 62 SRHGARYPTDSKKKYSALIEEIQQNATTFDGYKAFKTYNYSGLADLTTFEGEELVNS 121

Db SRHGARYPTDSKKKYSALIEEIQQNATTFDGYKAFKTYNYSGLADLTTFEGEELVNS 139

QY 122 GIKFYQYVESLTRNIVPIRSGSSRVIASGKFTIEGQSTKLKDPRAQPGSQSPKIDW 181

Db GIKFYQYVESLTRNIVPIRSGSSRVIASGKFTIEGQSTKLKDPRAQPGSQSPKIDW 199

QY 182 ISEASSNNTLDPGTCTVFEDSELADTVEANFTATFVSIQRLENDLSGYTLTDTEVY 241

Db ISEASSNNTLDPGTCTVFEDSELADTVEANFTATFVSIQRLENDLSGYTLTDTEVY 259

QY 242 LMDSCSFPTISTSTVDTKLSFPFCDLFTHDEWINDYLSLKKYCHGAGNPLGPTQGVY 301

Db LMDSCSFPTISTSTVDTKLSFPFCDLFTHDEWINDYLSLKKYCHGAGNPLGPTQGVY 301

```
Db      260 LMDMCSFDTISTSTVDTKLSPPCDLFTDHEWINVDYLSLKKYKHGAGNPLGPTQGVY 319
Qy      302 ANELIARLTHSPVHDDTSSNHTLDSSPATPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db      320 ANELIARLTHSPVHDDTSSNHTLDSSPATPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy      362 PLSTTTVENTITQDGFSSAWTVFPASRLYVEMMQCAEQBELVRLVNDVRVPLHGCPVD 421
Db      380 PLSTTTVENTITQDGFSSAWTVFPASRLYVEMMQCAEQBELVRLVNDVRVPLHGCPVD 439
Qy      422 ALGCRTRDSFVRGLSFARSGGDWAECA 449
Db      440 ALGCRTRDSFVRGLSFARSGGDWAECA 467

RESULT 2
JN0482
3-phytase (EC 3.1.3.8) A - Aspergillus ficum
N;Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phya protein
C;Species: Aspergillus ficum
C;Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: JN0482; PMID:1648914
R;Ullah, A.H.J.; Dischinger Jr., H.C.
Biochem. Biophys. Res. Commun. 192, 747-753, 1993
A;Title: Aspergillus ficum phytase: Complete primary structure elucidation by chemical
A;Reference number: JN0482; MUID:93249451; PMID:8387289
A;Accession: JN0482
A;Molecule type: protein
A;Residues: 1-441 <ULL>
A;Cross-references: UNIPROT:P34752
A;Note: authors state that the 9 Asn followed by Thr or Ser after an intervening residue
R;Ullah, A.H.J.; Cummins, B.J.; Dischinger Jr., H.C.
Biochem. Biophys. Res. Commun. 178, 45-53, 1991
A;Title: Cyclohexanediolone modification of arginine at the active site of Aspergillus fic
A;Reference number: PN0023; MUID:91298982; PMID:1648914
A;Accession: PN0023
A;Molecule type: protein
A;Residues: 48-70 <U12>
A;Comment: This enzyme catalyzes the hydrolysis of inorganic orthophosphate from phytate
C;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
F;4,36,82,97,184,207,316,329,353,365/Binding site: carboxylate (Asn) (covalent) #status
F;58,338/Active site: Arg, His #status predicted
F;59/Active site: His (phosphohistidine intermediate) #status predicted

Query Match          98.2%; Score 2315; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 3,4e-161;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 ASRNOSSCDTVDDGYQCFSETSHLWGOYAPFFSLANESVISPVPAGCRVTFQAQLSRHG 65
Db      1 ASRNOSSCDTVDDGYQCFSETSHLWGOYAPFFSLANESVISPVPAGCRVTFQAQLSRHG 60
Qy      66 ARYPTDSKGGKYSALIEEIQNATTFDGKYAFKTYNSLGGADLTTPFGEQLVNSGIKF 125
Db      61 ARYPTDSKGGKYSALIEEIQNATTFDGKYAFKTYNSLGGADLTTPFGEQLVNSGIKF 120
Qy      126 YQRYESTLRNIVPPIRSGSSSRVITAGKKFIEGQSTKLKDPRAQPGQSSPKIDVISEA 185
Db      121 YQRYESTLRNIVPPIRSGSSSRVITAGKKFIEGQSTKLKDPRAQPGQSSPKIDVISEA 180
Qy      186 SSSNNLTDPGCTVFEDSELADTVANFTATFVPSIRQRLENDLSGVTLTDTTEVTYLMDM 245
Db      181 SSSNNLTDPGCTVFEDSELADTVANFTATFVPSIRQRLENDLSGVTLTDTTEVTYLMDM 240
Qy      246 CSFDTISTSTVDTKLSPPCDLFTDHEWINVDYLSLKKYKHGAGNPLGPTQGVYANEL 305
Db      241 CSFDTISTSTVDTKLSPPCDLFTDHEWINVDYLSLKKYKHGAGNPLGPTQGVYANEL 300
Qy      306 IARLTHSPVHDDTSSNHTLDSSPATPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 365
Db      301 IARLTHSPVHDDTSSNHTLDSSPATPLNSTLYADFSHDNGIISILFALGLYNGTKPLST 360
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Qy      366 TTVENITQDGFSSAWTVFPASRLYVEMMQCAEQBELVRLVNDVRVPLHGCPVDALGR 425
Db      361 TTVENITQDGFSSAWTVFPASRLYVEMMQCAEQBELVRLVNDVRVPLHGCPVDALGR 420
Qy      426 CTRDSFVRGLSFARSGGDWAE 446
Db      421 CTRDSFVRGLSFARSGGDWAE 441

RESULT 3
JN0889
3-phytase (EC 3.1.3.8) A precursor - Aspergillus awamori
N;Alternate names: myo-inositol hexakisphosphate phosphohydrolase; phya protein
C;Species: Aspergillus awamori
C;Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: JN0889
R;Piddington, C.S.; Houston, C.S.; Paloheimo, M.; Cantrell, M.; Miettinen-Cinonen, A.; Ne
Gene 133, 55-62, 1993
A;Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-optim
A;Reference number: JN0889; MUID:94040796; PMID:8224894
A;Accession: JN0889
A;Molecule type: DNA
A;Residues: 1-467 <PID>
A;Cross-references: UNIPROT:P34753; GB:I02421; NID:G166518; PIDN:AAAL6898.1; PID:G166519
A;Experimental source: strain ALK0243
A;Note: part of the sequence, including the amino end of the mature protein, was confirme
C;Comment: This enzyme catalyzes the conversion of phytate to inositol and inorganic phos
C;Genetics:
A;Gene: phya
A;Introns: 15/2
C;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-467/Product: 3-phytase A #status experimental <MAT>
F;27,59,105,120,207,230,339,352,376,388/Binding site: carboxylate (Asn) (covalent) #stat
F;81,361/Active site: Arg, His #status predicted
F;82/Active site: His (phosphohistidine intermediate) #status predicted

Query Match          97.9%; Score 2309; DB 1; Length 467;
Best Local Similarity 97.3%; Pred. No. 1e-160;
Matches 436; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Qy      2 LAVPASRNOSSCDTVDDGYQCFSETSHLWGOYAPFFSLANESVISPVPAGCRVTFQAQL 61
Db      20 LAVPASRNOSSCDTVDDGYQCFSETSHLWGOYAPFFSLANESVISPVPAGCRVTFQAQL 79
Qy      62 SRHGARYPTDSKGGKYSALIEEIQNATTFDGKYAFKTYNSLGGADLTTPFGEQLVNS 121
Db      80 SRHGARYPTDSKGGKYSALIEEIQNATTFDGKYAFKTYNSLGGADLTTPFGEQLVNS 139
Qy      122 GIKFYQRYESTLRNIVPPIRSGSSSRVITAGKKFIEGQSTKLKDPRAQPGQSSPKIDVV 181
Db      140 GIKFYQRYESTLRNIVPPIRSGSSSRVITAGKKFIEGQSTKLKDPRAQPGQSSPKIDVV 199
Qy      182 ISEASSNNLTDPGCTVFEDSELADTVANFTATFVPSIRQRLENDLSGVTLTDTTEVTY 241
Db      200 ISEASSNNLTDPGCTVFEDSELADTVANFTATFVPSIRQRLENDLSGVTLTDTTEVTY 259
Qy      242 LMDMCSFDTISTSTVDTKLSPPCDLFTDHEWINVDYLSLKKYKHGAGNPLGPTQGVY 301
Db      260 LMDMCSFDTISTSTVDTKLSPPCDLFTDHEWINVDYLSLKKYKHGAGNPLGPTQGVY 319
Qy      302 ANELIARLTHSPVHDDTSSNHTLDSSPATPLNSTLYADFSHDNGIISILFALGLYNGTK 361
Db      320 ANELIARLTHSPVHDDTSSNHTLDSSPATPLNSTLYADFSHDNGIISILFALGLYNGTK 379
Qy      362 PLSTTTVENTITQDGFSSAWTVFPASRLYVEMMQCAEQBELVRLVNDVRVPLHGCPVD 421
Db      380 PLSTTTVENTITQDGFSSAWTVFPASRLYVEMMQCAEQBELVRLVNDVRVPLHGCPVD 439
Qy      422 ALGCRTRDSFVRGLSFARSGGDWAECA 449
Db      440 ALGCRTRDSFVRGLSFARSGGDWAECA 467
```

RESULT 4

PARYC

acid phosphatase (EC 3.1.3.2) repressible, precursor - yeast (*Saccharomyces cerevisiae*)
N/Alternate names: acid phosphatase PHO5; protein YBR0814; protein YBR093c
C/Species: *Saccharomyces cerevisiae*
C/Date: 19-Feb-1984 #sequence revision 30-Sep-1991 #text change 09-Jul-2004
C/Accession: S05795; S48260; S45961; A00777; A38793; S41855; B25241; A253367; A27
R; Bajwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinne, A.
Nucleic Acids Res. 12, 7721-7739, 1984
A/Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast
A/Reference number: S05794; MUID:85037940; PMID:6093051
A/Accession: S05795
A/Molecule type: DNA
A/Residues: 1-467 <BAJ>
A/Cross-references: UNIPROT:P06335; EMBL:X01079; NID:g4162; PIDN:CAA35555.1; PID:g758282
A/Note: the authors translated the codon TAC for residue 272 as Thr
A/Accession: A38792
A/Molecule type: protein
A/Residues: 18-45 <BAJ2>
R; Mannhaupt, G.; Stucka, R.; Ehnlé, S.; Vetter, I.; Feldmann, H.
Yeast 10, 1363-1381, 1994
A/Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A/Reference number: S48255; MUID:95208357; PMID:7900426
A/Accession: S48260
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-467 <WAN>
A/Cross-references: EMBL:X78993; NID:g476045; PIDN:CAA55598.1; PID:g476051
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
R; Feldmann, H.; Mannhaupt, G.; Schwarzlöse, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A/Reference number: S45927
A/Accession: S45961
A/Molecule type: DNA
A/Residues: 1-467 <FE2>
A/Cross-references: EMBL:X235962; NID:g536364; PIDN:CAA85046.1; PID:g536365; GSPDB:GN00000
R; Arima, K.; Oshima, T.; Kubota, I.; Nakamura, N.; Mizunaga, T.; Toh-e, A.
Nucleic Acids Res. 11, 1657-1672, 1983
A/Title: The nucleotide sequence of the yeast PHO5 gene: a putative precursor of repress
A/Reference number: A00777; MUID:83168913; PMID:6300772
A/Accession: A00777
A/Molecule type: DNA
A/Residues: 1-35, 'Y', 37-129, 'G', 131-293, 'Q', 295-445, 'V', 447-461, 'DT', 464-465, 'K', 467 <AR
A/Cross-references: EMBL:V01320; NID:g4158; PIDN:CAA24630.1; PID:g4159
A/Accession: A38793
A/Molecule type: protein
A/Residues: 18-26, 'X', 28 <ARI2>
R; Meyhack, B.; Bajwa, W.; Rudolph, H.; Hinne, A.
EMBO J. 1, 675-680, 1982
A/Title: Two yeast acid phosphatase structural genes are the result of a tandem duplicat
A/Reference number: S41855; MUID:84236032; PMID:6329697
A/Accession: S41855
A/Molecule type: DNA
A/Residues: 1-30, 'T', 32-51, 'S', 53-75 <MEV>
A/Cross-references: EMBL:M24178; NID:g172156; PIDN:AAA34868.1; PID:g172157
R; Tai-Kamrat, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Thill, G.
Mol. Cell. Biol. 6, 1855-1865, 1986
A/Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within
A/Reference number: A93074; MUID:87064474; PMID:3537710
A/Accession: B25241
A/Molecule type: DNA
A/Residues: 1-44 <TAI>
R; Bergman, L.W.
Mol. Cell. Biol. 6, 2298-2304, 1986
A/Title: A DNA fragment containing the upstream activator sequence determines nucleosome
A/Reference number: A25367; MUID:87064526; PMID:3023927
A/Accession: A25367
A/Molecule type: DNA
A/Residues: 1-2, 'Y', 4-43, 'T', 45-51 <BER>
R; Silve, S.; Monod, M.; Hinne, A.; Hagenauer-Tsapis, R.
Mol. Cell. Biol. 7, 3306-3314, 1987

A>Title: The yeast acid phosphatase can enter the secretory pathway without its N-terminin

A/Reference number: A27774; MUID:89036886; PMID:3313013

A/Accession: A27774

A/Molecule type: DNA

A/Residues: 1-51,'S',53-60 <SIL>

A/Cross-references: GB:M:7306

C/Genetics:

A/Gene: SGD:PHO5; MIPS:YBR093C

A/Cross-references: SGD:S0000297; MIPS:YBR093C

A/Map position: 2R

A/Note: YBR093C

C/Superfamily: yeast acid phosphatase

C/Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrolas

F/1-17/Domain: signal sequence #status predicted <Sig>

F/18-467/Product: acid phosphatase, repressible #status experimental <MAT>

F/75/Active site: His (phosphohistidine intermediate) #status predicted

F/97,103,162,192,250,315,356,390,439,445,456,461/Binding site: carbohydrate (Asn) (coval

F/337/Active site: His #status predicted

Query Match 16.3%; Score 385; DB 1; Length 467;
Best Local Similarity 26.2%; Pred. No.2.4e-20;
Matches 114; Conservative 66; Mismatches 189; Indels 66; Gaps 14;

Qy 31 GOYAPFSLANESVTSPEVPAGCRVTFQAQLSRHGARYPTDSKGGKYSAIIEIQNAIT 90
Db :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Dy 42 GGAGFYYSFGDYGISRDLPCEGMKQLQMVRHGERYPYTVSLAKTIKSTWYKLSNYTRQ 101
Qy 91 FDGKYAFLK-TYNYSLGADD-----LTPF-GEQELVNSGIKFQRYESLTR 134
Db :|::||::||::||::||::||::||::||::||::||::||::||::||
Dy 102 FNGSLFLNDYEFIRDDDDLEMETTANSDDVLNPTYGENNAKHARDFLAQGYMVE 161
Qy 135 NIVPF-IRSSGSSRVIASGKKFIQGFQSTKLDPRAQQSQSPKIDVVISEASSNNLTLD 193
Db :|::||::||::||::||::||::||::||::||::||::||::||::||
Dy 162 NQTSEAVFTSNKRCHDTAIFYIDG-----LGD-----QFNITLTQVSEAESAGANTLS 210
Qy 194 P-GTCVFDESELADTVEANTATFPVPSIORLENLDSGLVTLTDEVTYIMDMCSFDTIS 252
Db :|::||::||::||::||::||::||::||::||::||::||::||::||
Dy 211 ACNSCPAW-DYDANDDI VNEYDITYLLDDIAKLKENKGLNLTTSDASTLFSGWCAFE--- 266
Qy 253 TSTVDTK-LSPFCDLFTHEMINVDYLQSLKKYGHGAGNPLGPTQGVAYNELIALRLTH 311
Db :|::||::||::||::||::||::||::||::||::||::||::||::||
Dy 267 ---VNAGYSDVCDFIKDELHVLYSYQDLHTYHEGPGYDI IKSVGSNFLFNASVKLLKQ 323
Qy 312 SPVHDDTSSNHTLSDSPATFLNLTLYADFHDNGII SILFALGLYNGTKPLSTTTVENI 371
Db :|::||::||::||::||::||::||::||::||::||::||::||::||
Dy 324 SEIOD-----QKVLSFTHTDILNFLLTAGIIDDKNNLTAEVVPFM 365
Qy 372 TOTDGFSANTVPPASRIYVMQCQAEPLRVLVLRVNDRVVPLHGCPVDALGRCTRDSGF 431
Db :|::||::||::||::||::||::||::||::||::||::||::||::||
Dy 366 GNT--FHRSWMVPOGARVYTEKFCQ--SNDTVRVYVINDAVVPIETCTSGPGFSCEINDF 421
Qy 432 -----VRGLSEAR 439
Db :|::||::||::||::||::||::||::||::||::||::||::||::||
Dy 422 YDAEKKVAGTDFFLK 436

RESULT 5
PABYCC

acid phosphatase (EC 3.1.3.2) precursor, constitutive - yeast (*Saccharomyces cerevisiae*)
N/Alternate names: acid phosphatase PHO3; protein YBR0813; protein YBR092c
C/Species: *Saccharomyces cerevisiae*
C/Date: 30-Sep-1991 #sequence revision 09-Sep-1994 #text_change 09-Jul-2004
C/Accession: S48259; S45960; S05794; A25241; S44674
R/Mannhaupt, G.; Stucka, R.; Ehle, S.; Vetter, I.; Feldmann, H.
Yeast 10, 1363-1381, 1994
A/Title: Analysis of a 70 kb region on the right arm of yeast chromosome II.
A/Reference number: S48255; MUID:95208357; PMID:7900426
A/Accession: S48259
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-467 <MAN>
A/Cross-references: UNIPROT:P24031; EMBL:X78993; NID:g476045; PIDN:CAA55597.1; PID:g47605
A/Note: the nucleotide sequence was submitted to the EMBL Data Library. April 1994

R;Pelkmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45927
A;Accession: S45960
A;Molecule type: DNA
A;Residues: 1-467 <FE2>
A;Cross-references: EMBL:Z35961; NID:G536362; PIDN:CAA85045.1; PID:G536363; GSPDB:GN0000
R;Bajwa, W.; Meyhack, B.; Rudolph, H.; Schweingruber, A.M.; Hinnen, A.
Nucleic Acids Res. 12, 7721-7739, 1984
A;Title: Structural analysis of the two tandemly repeated acid phosphatase genes in yeast
A;Reference number: S05794; MUID:85037940; PMID:6093051
A;Accession: S05794
A;Molecule type: DNA
A;Residues: 1-218, 'NKT', 222-467 <BAJ1>
A;Cross-references: EMBL:X01080; NID:G4148; PIDN:CAA25557.1; PID:G758281
A;Note: the authors translated the codon AAT for residue 134 as Asp and TAC for residue
R;Tait-Kaurat, A.G.; Turner, K.J.; Kramer, R.A.; Elliott, Q.D.; Bostian, S.J.; Thill, G.
Mol. Cell. Biol. 6, 1855-1865, 1986
A;Title: Reciprocal regulation of the tandemly duplicated PHO5/PHO3 gene cluster within
A;Reference number: A93074; MUID:87064474; PMID:3537710
A;Accession: A25241
A;Molecule type: DNA
A;Residues: 1-44 <TAI>
C;Genetics:
A;Gene: SGD:PHO3; MIPS:YBR092C
A;Cross-references: SGD:S0000296; MIPS:YBR052C
A;Map position: 2R
C;Superfamily: yeast acid phosphatase
C;Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrola
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-467/Product: acid phosphatase, constitutive #status predicted <MAT>
F;75/Active site: His (phosphohistidine intermediate) #status predicted
F;97, 103, 162, 192, 250, 315, 356, 390, 439, 445, 456, 461/Binding site: carbohydrate (Asn) (coval
F;337/Active site: His #status predicted
Query Match 16.3%; Score 385; DB 1; Length 467;
Best Local Similarity 26.1%; Pred. No. 2.4e-20;
Matches 113; Conservative 63; Mismatches 195; Indels 62; Gaps 11;
QY 31 GQVAPFSLANESVISPVPAGCRVTFQVLSHGARYPTDSKGYKYSALIEIQNATT 90
Db 42 GGAGPYFPPGDIYISRDLEPGCEMKQLQMLARHGERTYPTYSKATIMKTWYKLSNYTRQ 101
QY 91 FDGKYAFLK-TYNSVLCADD-----LTPF-GEQLVNSGKIFQYRYSLTR 134
Db 102 FNGSLFLNDYDFFTRDDDDLEMETTFANSNDVLPYTGEMAKRHAREFLAQGYMFE 161
QY 135 NIVFP-IRSSGSRVITAGKKFIEGFQSTKLKDPRAQPGSQSPKIDVIVISEASSNNITLD 193
Db 162 NQTSFPIFAASRVRVHTAQYFIDG-----LGD-----QFNISLQTVSEAMGAGANTLS 210
QY 194 PGCTVPEDSELADTVENATFATFVPSIRQRLNDLSGVTLTTEVTYLMDCSFDTIST 253
Db 211 AGNACPGWDENDDDLDKDYDTTLLDIAKLNKNGKLNLTSKDANTLFAWCAYELNAR 270
QY 254 STVDTKLSPPCDLFTDHEWNYDYLSQSLKYYGHGAGNPLGPTQGVGYANELIARLTHSP 313
Db 271 GYSDV-----CDLFTDELVRYSYQDLVSYQDGPYDMIRSVGANLFWATLKLKQSE 325
QY 314 VHDTSNHWLDSPPATFPLNSTLYADFSHNGIISILFALGLYNGKPKLSTTTVENITQ 373
Db 326 TQD-----LKVLSFTHTDITLNYLTLAGIIDDKNNLTAETVPPMGN 367
QY 374 TDGFSASWTPFASRLVEMWQCAEQEPLVRVLVNDRVPLHGPCPVDALGRCTRDSF-- 431
Db 368 T--FKSWYVPGQARVYTEKFCQ--SNDTVRVVINDAVVPIETCTCGPGFSCEINDFYD 423
QY 432 -----VRGLSFAR 439
Db 424 YAEKRVAGTDFLK 436

RESULT 6

S52495
acid phosphatase homolog YDL024c - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein D2815
C;Species: Saccharomyces cerevisiae
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52495; S67556
R;Andre, B.; Visser, S.; Urrestarazu, L.
submitted to the EMBL Data Library, February 1995
A;Description: The sequence of a 42 kb segment located on the left arm of chromosome IV i
A;Reference number: S52492
A;Accession: S52495
A;Molecule type: DNA
A;Residues: 1-468 <AND>
A;Cross-references: UNIPROT:P52290; EMBL:Z48432; NID:G683669; PIDN:CAA88335.1; PID:G68366
R;Urrestarazu, L.A.; Andre, B.; Visser, S.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67535
A;Accession: S67556
A;Molecule type: DNA
A;Residues: 1-468 <URR>
A;Cross-references: EMBL:Z74072; NID:G1430996; PIDN:CAA98583.1; PID:G1430997; MIPS:YDL024
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:DIA3
A;Cross-references: SGD:S0002182
A;Map position: 4L
C;Superfamily: yeast acid phosphatase
Query Match 15.6%; Score 368; DB 2; Length 468;
Best Local Similarity 25.0%; Pred. No. 4.2e-19;
Matches 109; Conservative 74; Mismatches 181; Indels 72; Gaps 13;
QY 31 GQVAPFSLANESVISPVPAGCRVTFQVLSHGARYPTDSKGYKYSALIEIQNATT 90
Db 43 GGSAPYFPPANYGIFTDPEGCRLTQVQMTGHRGERTYPTSEAKDIFEVYKISNYTKG 102
QY 91 FDGKYAFLLK-TYNSL-----GADDLTPF-GEQLVNSGKIFQYRYSLTR 134
Db 103 YEGSLFLNGYEFFIPDESLLMETTLQNSIDVLPYTGEMAKRHAREFLAKYKGLME 162
QY 135 NIVFP-IRSSGSRVITAGKKFIE---GPQSTKLKDPRAQPGSQSPKIDVIVISEASSN 189
Db 163 NCTNPFIFTNSKRIYDTAQYFAEALGDGFNIS-----LQTLSENSGA 207
QY 190 NTLDPCTVPEDELADTVENATFATFVPSIRQRLNDLSGVTLTTEVTYLMDCSPD 249
Db 208 NTLAAKSSCPNWSNANNIDILMSYSDLENISDRNDENKLNLSKDAALFSCWCFE 267
QY 250 TISTSTVDTK-LSPPFCDFLTHDEWNYDYLSQSLKYYGHGAGNPLGPTQGVGYANELIAR 308
Db 268 -----LNAGYGNICDIFSAELIHYSETDLTSFQNGPGYKLIKISGANLFNATV-K 320
QY 309 LTHSPVHDDTSNHTLDSPPATFPLNSTLYADFSHNGIISILFALGLYNGKPKLSTTTV 368
Db 321 LIRQSAH-----LBQKWLSTHTDITLNYLTLAGIIDDKNLTNNHV 363
QY 369 ENITQDGFSSAWTPFASRLVEMWQCAEQEPLVRVLVNDRVPLHGPCPVDALGRCTR 428
Db 364 P--FRDHSYHRSWYIFQGARVYTEKFCQ--SNDSYRVVNDVAVFIESCSSGPGFSCEE 419
QY 429 DSF-----VRGLSF 437
Db 420 GTFEYVAKDLRLGVSF 435

RESULT 7

S48996
acid phosphatase (EC 3.1.3.2) PHO12 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YHR215W
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: S48996; S59659

R;Macri, C.
 submitted to the EMBL Data Library, February 1994
 A;Description: The sequence of *S. cerevisiae* cosmid 9177.
 A;Reference number: S46671
 A;Accession: S48996
 A;Molecule type: DNA
 A;Residues: 1-467 <MAC>
 A;Cross-references: UNIPROT:P38693; EMBL:U00029; NID:g551322; PIDN:AA69729.1; PID:g4589
 R;Xu, L.
 submitted to the EMBL Data Library, January 1995
 A;Reference number: S59658
 A;Accession: S59659
 A;Molecule type: DNA
 A;Residues: 1-16,'L',18-81,'AR',84-149,'H',151-467 <XUL>
 A;Cross-references: EMBL:U19789; NID:g847754; PIDN:AAA73479.1; PID:g847755
 C;Genetics:
 A;Gene: SGD:PHO12
 A;Cross-references: SGD:S0001258; MIPS:YHR215W
 A;Map position: 8R
 C;Superfamily: yeast acid phosphatase
 C;Keywords: phosphoric monoester hydrolase

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Query Match          14.9%; Score 352; DB 2; Length 467;
Best Local Similarity 24.4%; Pred. No. 6.1e-18;
Matches 107; Conservative 70; Mismatches 189; Indels 72; Gaps 14;

QY 31 GQYAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARYPTDSKGKYSALIEEQNATT 90
Db 42 GSGPYVFPDGYGISRDLPESCCKQVQVGRHGERPTTVSKAKSINTWYKLSNYTGG 101

QY 91 FDGKYAFILK-----TYNYSL-----GADDLTPF-GEQELVNSGKIFYQYESLTR 134
Db 102 FSGALSFLNDDYEFPIRDTKNLEMETTLANSVNLNPTVTGEMNAKRHARDFLAQGYMVE 161

QY 135 NIVPP-IRSSGSRVIAAGKGFIEGFQSTKLDKPAQPGQSSPKIDV---VISEASSN- 189
Db 162 NQTSFAVFTSNRCHDTAQYFIDGL-----GDKFNIQLQITSEASAGA 206

QY 190 NTLDP-GCTVFESDELADTVEANFTATFVPSIRORLENDLSGVTLTDTTEVYLMDCSF 248
Db 207 NTLSAHSCPAWDD-DVNDLILKDYTKYLSGIARLNKENKGLNLTSSDANTFFAWCAY 265

QY 249 DTISTVDTKLSPPCDLFTHDEWINDYQLSKKYYGHGAGNPLGPTQGVGYANELIAR 308
Db 266 EINARG-----YSDICNIFTKDELVRFSYGQDLETYYQTGPGYDVRSVGANLFNASVKL 320

QY 309 LTHSPVHDTSNHTLSDSPATFPLNSTLYADPSHDNGIISILFALGLYNGTKPLSTTV 368
Db 321 LKESVQD-----QKWLSTHTDITLNYLTITIGIDDKNNLTAEHV 362

QY 369 ENITQDGFSSAWTPPFASRLYVEMMQCAEQEPLRVLVNDRVPLHGCPCVDALGRCTR 428
Db 363 PFMENT--FHSWVYVPGARVYTEKFC--SNDYVVRVINDAVVPIETCTSGPGFSCEI 418

QY 429 DSP-----VRGLSFAR 439
Db 419 NDFYGYAEKRVAGTDFLK 436

```

RESULT 8
 S53476
 3-phytase (EC 3.1.3.2) precursor - yeast (*Saccharomyces cerevisiae*)
 N;Alternate names: protein YAR071w
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 05-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
 C;Accession: S53476; JCI018
 R;Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Kabac
 submitted to the EMBL Data Library, February 1994
 A;Description: Sequencing of chromosome I of *Saccharomyces cerevisiae*: analysis of the 5
 A;Reference number: S53458
 A;Accession: S53476
 A;Molecule type: DNA
 A;Residues: 1-467 <BUS>

A;Cross-references: UNIPROT:P35842; EMBL:L28920; NID:g1616966; PIDN:AA09508.1; PID:g4561
 R;Chen, J.Y.; Gong, Y.; Ao, S.Z.
 Acta Biochim. Biophys. Sin. 21, 437-444, 1989
 A;Title: The primary structure of acid phosphatase gene PHO11 in *S. cerevisiae* and compa
 A;Reference number: JCI018
 A;Accession: JCI018
 A;Molecule type: DNA
 A;Residues: 1-16,'L',18-149,'H',151-353,'O',355-422,'G',424-467 <CHE>
 A;Note: this paper is in Chinese, with an English abstract
 C;Genetics:
 A;Gene: SGD:PHO11
 A;Cross-references: SGD:S0000094; MIPS:YAR071w
 A;Map position: 1R
 C;Superfamily: yeast acid phosphatase
 C;Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrolase
 F;1-17/Domain: signal sequence #status predicted <SIG>
 F;18-467/Product: acid phosphatase #status predicted <MAT>
 F;74/Active site: Arg #status predicted
 F;75/Active site: His (phosphohistidine intermediate) #status predicted
 F;97,162,192,250,315,356,439,445,461/Binding site: carboxylate (Asn) (covalent) #status

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Query Match          14.9%; Score 352; DB 2; Length 467;
Best Local Similarity 24.4%; Pred. No. 6.1e-18;
Matches 107; Conservative 70; Mismatches 189; Indels 72; Gaps 14;

QY 31 GQYAPFFSLANESVISPEVPAGCRVTFQAQLSRHGARYPTDSKGKYSALIEEQNATT 90
Db 42 GSGPYVFPDGYGISRDLPESCCKQVQVGRHGERPTTVSKAKSINTWYKLSNYTGG 101

QY 91 FDGKYAFILK-----TYNYSL-----GADDLTPF-GEQELVNSGKIFYQYESLTR 134
Db 102 FSGALSFLNDDYEFPIRDTKNLEMETTLANSVNLNPTVTGEMNAKRHARDFLAQGYMVE 161

QY 135 NIVPP-IRSSGSRVIAAGKGFIEGFQSTKLDKPAQPGQSSPKIDV---VISEASSN- 189
Db 162 NQTSFAVFTSNRCHDTAQYFIDGL-----GDKFNIQLQITSEASAGA 206

QY 190 NTLDP-GCTVFESDELADTVEANFTATFVPSIRORLENDLSGVTLTDTTEVYLMDCSF 248
Db 207 NTLSAHSCPAWDD-DVNDLILKDYTKYLSGIARLNKENKGLNLTSSDANTFFAWCAY 265

QY 249 DTISTVDTKLSPPCDLFTHDEWINDYQLSKKYYGHGAGNPLGPTQGVGYANELIAR 308
Db 266 EINARG-----YSDICNIFTKDELVRFSYGQDLETYYQTGPGYDVRSVGANLFNASVKL 320

QY 309 LTHSPVHDTSNHTLSDSPATFPLNSTLYADPSHDNGIISILFALGLYNGTKPLSTTV 368
Db 321 LKESVQD-----QKWLSTHTDITLNYLTITIGIDDKNNLTAEHV 362

QY 369 ENITQDGFSSAWTPPFASRLYVEMMQCAEQEPLRVLVNDRVPLHGCPCVDALGRCTR 428
Db 363 PFMENT--FHSWVYVPGARVYTEKFC--SNDYVVRVINDAVVPIETCTSGPGFSCEI 418

QY 429 DSP-----VRGLSFAR 439
Db 419 NDFYGYAEKRVAGTDFLK 436

```

RESULT 9
 JN0715
 3-phytase (EC 3.1.3.8) B precursor - *Aspergillus ficum*
 N;Alternate names: pH 2.5-optimum acid phosphatase
 C;Species: *Aspergillus ficum*
 C;Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
 C;Accession: JN0715; FN0594; FN0460
 R;Ehrlich, K.C.; Montalbano, B.G.; Mullaney, E.J.; Dischinger Jr., H.C.; Ullah, A.H.J.
 Biochem. Biophys. Res. Commun. 195, 53-57, 1993
 A;Title: Identification and cloning of a second phytase gene (phyB) from *Aspergillus nigr*
 A;Reference number: JN0715; MUID:93371452; PMID:7916610
 A;Accession: JN0715
 A;Molecule type: DNA
 A;Residues: 1-479 <EHR>
 A;Cross-references: UNIPROT:P81440; GB:L20567

A;Accession: PN0594
A;Molecule type: protein
A;Residues: 20-101;133-146;376-399 <RH2>
R;Ullah, A.H.J.; Dischinger Jr., H.C.
Biochem. Biophys. Res. Commun. 192, 754-759, 1993
A;Title: Identification of active-site residues in Aspergillus ficum extracellular pH 2
A;Reference number: PN0460; MUID:93249452; PMID:8484781
A;Accession: PN0460
A;Molecule type: protein
A;Residues: 65-66,68-93 <ULL>
C;Comment: This enzyme, previously characterized as an acid phosphatase (EC 3.1.3.2), has
C;Genetics:
A;Gene: phyB
A;Introns: 261/1; 300/2; 335/2
C;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-479/Product: 3-phytase #status experimental <MAT>
F;81,337/Active site: Arg, His #status predicted
F;92/Active site: His (phosphohistidine intermediate) #status predicted
F;106,191,227,250,315,340,425,442,458/Binding site: carboxylate (Asn) (covalent) #statu

Query Match 14.4%; Score 339.5; DB 1; Length 479;
Best Local Similarity 27.0%; Pred. No. 5.2e-17;
Matches 118; Conservative 64; Mismatches 186; Indels 69; Gaps 19;
QY 3 AVPASRNQSS-CUTVQGYQCFSETSHLWQYAPFFSLANESV---ISPEVPAGCRVTPA 58
Db 25 AIPQSTQEKQFQSEFRDGYSLKH---YGGNGPY---SERVSYGIARDPPTGCEVDQV 76
QY 59 QVLSRHGARYPTDSKGGKY-SALIEEIQQNATTFDGYAFKTYNYSL-----GADDLT 111
Db 77 IMVRRHGERYPSPSAGKSIIEALAKVYSINTYKGDALFNDWTYYVNECYNAETTS 136
QY 112 -PF-GEQELVNSGKIFQRYESL--TRNIVPFISSGSSRVIASGKFFIEGPOSTKLKDP 167
Db 137 GPVAGLLDAYNHGNDYKARYGHLWNGETVVVFPF--SSGYGRVETARKFGEGFGYNY-- 192
QY 168 RAOPGQSSPKIDVVISSEASSNNTLDPGCTVPEDESELADTVEANFTATVPSTQRLN 227
Db 193 -----STNAALNIISSEVMGADSLTP--TCDTNDQTTCDNLTYQLPQFKVAARLNSQN 246
QY 228 DLGVTLTDTETVYLMDCSFDTISTSTVDTKLSPFCDLFTHDEWINDYLSLKYYGH 287
Db 247 --PGMNLITASDVNLMVMASFELNA-----RPSNWINATQDEWVSGFVEDLNYICA 299
QY 288 GAGNPLGPTQGVYANELIARLTHSPVHDDTSSNHTLDSSPATPPLNSTLYADPSSHNGI 347
Db 300 GPGDKMAAVGAVYANASLTLLNQGP-----KEAGP-----LFFNLADHTNI 341
QY 348 ISILFALGLY--NGTKPLSTTTVENTITQDFSSAWTPFASRLYVEMMOCA-----EQE 401
Db 342 TPILAALGLVLPNEDLPLDRVAFGN-----PYSIGNIVPMGGHLLTIERLSQATALSDEK 396
QY 402 PLVRLVNDRVVPLHGC 418
Db 397 TYVRLVNEAVLPFND 413

RESULT 10
JN0890
acid phosphatase (EC 3.1.3.2) precursor - Aspergillus awamori
C;Species: Aspergillus awamori
C;Date: 14-Jul-1994 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: JN0890
R;Piddington, C.S.; Houston, C.S.; Palohimo, M.; Cantrell, M.; Miettinen-Oinonen, A.; N
Gene 133, 55-62, 1993
A;Title: The cloning and sequencing of the genes encoding phytase (phy) and pH 2.5-opti
A;Reference number: JN0889; MUID:94040796; PMID:8224894
A;Accession: JN0890
A;Molecule type: DNA
A;Residues: 1-479 <PID>
A;Cross-references: UNIPROT:P34755; GB:L02420; NID:g166481; PIDN:AAA16897.1; PID:g166482

A;Experimental source: strain ALX0243
C;Comment: The highly similar enzyme from A. ficum has been shown to have 3-phytase (EC
C;Genetics:
A;Gene: aph
A;Introns: 261/1; 300/2; 335/2
C;Superfamily: yeast acid phosphatase
C;Keywords: extracellular protein; glycoprotein; phosphohistidine; phosphoprotein; phosph
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-479/Product: 3-phytase #status predicted <MAT>
F;81,337/Active site: Arg, His #status predicted
F;92/Active site: His (phosphohistidine intermediate) #status predicted
F;106,191,227,250,315,340,425,442,458/Binding site: carboxylate (Asn) (covalent) #statu

Query Match 14.4%; Score 338.5; DB 1; Length 479;
Best Local Similarity 26.8%; Pred. No. 6.1e-17;
Matches 117; Conservative 63; Mismatches 188; Indels 69; Gaps 18;
QY 3 AVPASRNQSS-CUTVQGYQCFSETSHLWQYAPFFSLANESV---ISPEVPAGCRVTPA 58
Db 25 AIPQSTQEKQFQSEFRDGYSLKH---YGGNGPY---SERVSYGIARDPPTSCHEVDQV 76
QY 59 QVLSRHGARYPTDSKGGKY-SALIEEIQQNATTFDGYAFKTYNYSL-----GADDLT 111
Db 77 IMVRRHGERYPSPSAGKSIIEALAKVYSINTYKGDALFNDWTYYVNECYNAETTS 136
QY 112 -PF-GEQELVNSGKIFQRYESL--TRNIVPFISSGSSRVIASGKFFIEGPOSTKLKDP 167
Db 137 GPVAGLLDAYNHGNDYKARYGHLWNGETVVVFPF--SSGYGRVETARKFGEGFGYNY-- 192
QY 168 RAOPGQSSPKIDVVISSEASSNNTLDPGCTVPEDESELADTVEANFTATVPSTQRLN 227
Db 193 -----STNAALNIISSEVMGADSLTP--TCDTNDQTTCDNLTYQLPQFKVAARLNSQN 246
QY 228 DLGVTLTDTETVYLMDCSFDTISTSTVDTKLSPFCDLFTHDEWINDYLSLKYYGH 287
Db 247 --PGMNLITASDVNLMVMASFELNA-----RPSNWINATQDEWVSGFVEDLNYICA 299
QY 288 GAGNPLGPTQGVYANELIARLTHSPVHDDTSSNHTLDSSPATPPLNSTLYADPSSHNGI 347
Db 300 GPGDKMAAVGAVYANASLTLLNQGP-----AGSLFFNPAHDTNI 341
QY 348 ISILFALGLY--NGTKPLSTTTVENTITQDFSSAWTPFASRLYVEMMOCA-----EQE 401
Db 342 TPILAALGLVLPNEDLPLDRVAFGN-----PYSIGNIVPMGGHLLTIERLSQATALSDEG 396
QY 402 PLVRLVNDRVVPLHGC 418
Db 397 TYVRLVNEAVLPFND 413

RESULT 11
JC4285
acid phosphatase (EC 3.1.3.2) precursor - yeast (Pichia pastoris)
N;Alternate names: orthophosphoric monoester phosphohydrolase (acid optimum); Pho
C;Species: Pichia pastoris
C;Date: 14-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4285
R;Payne, W.E.; Gannon, P.M.; Kaiser, C.A.
Gene 163, 19-26, 1995
A;Title: An inducible acid phosphatase from the yeast Pichia pastoris: Characterization
A;Reference number: JC4285; MUID:96001238; PMID:7557473
A;Accession: JC4285
A;Molecule type: DNA
A;Residues: 1-468 <PAY>
A;Cross-references: UNIPROT:P52291; GB:U28658; NID:g881955; PIDN:AAA85503.1; PID:g881956
A;Experimental source: GS115
C;Genetics:
A;Gene: phoI
C;Superfamily: yeast acid phosphatase
C;Keywords: glycoprotein; phosphohistidine; phosphoprotein; phosphoric monoester hydrolyta
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-468/Product: acid phosphatase #status predicted <MAT>
F;84/Active site: His (phosphohistidine intermediate) #status predicted

QY 250 TISTSTVDTKLSPPCDLFTDHEWYNYDYLQSLKKYKHGAGNPLGPTQGVGYNELIARL 309
Db 268 IAIKHSDD-----FCSIFTPSEFLNFEYDSDDLQAYGGGPVSEWASTLGGAYINNUA--- 319
QY 310 THSPVHDDTSSNHTLSSPATFLNLTLYADFGHNGIISILFALGLYNGTKPLSTTTVE 369
Db 320 -----DSLERNVT---NP---DFDRKVFIAFTHDSNLIIPVEALGFFPDITQNPPLPTD 366
QY 370 NITQTDGSSAWTVPPASRLYVENMQCAEQEPLVRVLRVNDVRVPLHGC 418
Db 367 KNIITYTSQKTSFVPAGNLITELFFC-SDSKYVYRHLVNOQVYPLTDC 414

RESULT 14
S14119
acid phosphatase (EC 3.1.3.2) - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S14119; T40455
R:Yang, J.; Schweingruber, M.E.
Curr. Genet. 18, 269-272, 1990
A:Title: The structural gene coding for thiamin-repressible acid phosphatase in Schizosaccharomyces pombe
A:Reference number: S14119; MUID:91064763; PMID:2249257
A:Accession: S14119
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-463 <YAN>
A:Cross-references: UNIPROT:Q01682; GB:X56939; NID:g5006; PID:CAA40258.1; PID:g5007
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K.
submitted to the EMBL Data Library, November 1998
A:Reference number: Z21931
A:Accession: T40455
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-463 <YAN>
A:Cross-references: EMBL:AL034382; PIDN:CAA22278.1; GSPDB:GN00067; SPDB:SPBC428.03c
A:Experimental source: strain 972h-; cosmid c428
C:Genetics:
A:Gene: SPBC428.03c
A:Map position: 2
C:Superfamily: yeast acid phosphatase
C:Keywords: phosphoric monoester hydrolase

Query Match 12.08; Score 284; DB 2; Length 463;
Best Local Similarity 24.94; Pred. No. 5.5e-13;
Matches 102; Conservative 66; Mismatches 181; Indels 60; Gaps 13;
QY 33 YAPFFSLANBSVISPEVPAGCRVTFQAQVLSRHGARYP-----TDSKGGKYSALIE----- 82
Db 43 HEFYENGPTTS-----FPESCAIKQVHLLQRHGSRNPTGDDTATDVSSAQYIDIFQNKLL 97
QY 83 --FIQQNATTFDQKIAFLKYNYSL-----GADDLTPFGQEQLVNSGKIFQYQYRSLTRNIV 137
Db 98 NGSTIPVNFSPENPLYKVKWHTPVKAENADQLSSGRIELFDLGRQVFRYRYELFPTDV 157
QY 138 PFTRSSGSSVIASGKXFIQGFQSTKLDKPPAQGGQSSPKIDVVI---SEASSNNLTDP 194
Db 158 YDINTAQERVDSAEVFSYGMFGDDMON-----KTNFIVLDEDDSAGANSAMY 207
QY 195 GTCTVFEDSEL-ADTVEANFTA---TFVPSIRQLENDL-SGVTLTDTETVYLMDCMSFD 249
Db 208 YSCPVEDNNIDENTTEAAHSTWENVFLKPIANLKNKYFDSGYNLTVSDVRSLYICVYE 267
QY 250 TISTSTVDTKLSPPCDLFTDHEWYNYDYLQSLKKYKHGAGNPLGPTQGVGYNELIARL 309
Db 268 IALRDNDS-----FCSLFTSEFLNFEYDSDDLQAYWGGPASEWASTLGGAYVNNLANNL 322
QY 310 THSPVHDDTSSNHTLSSPATFLNLTLYADFGHNGIISILFALGLYNGTKPLSTTTVE 369
Db 323 R-----KGVNNASDRK-----VFIAFTHDSQIIPVEALGFFPDITPHEPLPTD 366
QY 370 NITQTDGSSAWTVPPASRLYVENMQCAEQEPLVRVLRVNDVRVPLHGC 418

Db 367 KNIITYSLKTSFVPAGNLITELFFC-SDKNKYVYRHLVNOQVYPLTDC 414

RESULT 15
A86233
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: A86233
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86233
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-468 <STO>
A:Cross-references: UNIPROT:O04509; GB:AE005172; NID:g2160177; PIDN:AAB60740.1; GSPDB:GN00067
C:Genetics:
A:Map position: 1
C:Superfamily: yeast acid phosphatase

Query Match 6.3%; Score 148; DB 2; Length 468;
Best Local Similarity 21.8%; Pred. No. 0.0047;
Matches 100; Conservative 60; Mismatches 202; Indels 96; Gaps 19;
QY 16 VDQYQCFSETSL--WGQYAPFSLANBSVISPEVPAGCRVTFQAQVLSRHGARYP--- 70
Db 16 VSQADQGFDRHSLTIVTRYSTSKDVTQNLIEGNNVPECTPHLLNLVASHGTRSPPKR 75
QY 71 ----DSKGGKYSALIEEIQNATTFDQKVAFL---KTNYSLGADDLTPFGQEQLVNSG 122
Db 76 LRELSLAGRFKLVDRDAERKLPSDKIPGWLQWKSFWEGKVGKGLIFQGEDELYQLG 135
QY 123 IKFYQRYESLTRN----IVFFIRSSGSSRVIAAGKXFIQGFQSTKLDKPPAQGGQSSPKI 178
Db 136 IRVRETFPSLFEEDYHFDVVTIRATQIPRASASAVAFGMGLFSEK---GNLGFGRN--RA 190
QY 179 DVVISASSNNVLDPECTCTVFEDS-----ELADTVEANFTATFVPSIRQLEND 228
Db 191 FAVTSENRASDTKLRFECQNYKSYRKAKEPAVDKLEPVLNKITA----SVAKRID-- 244
QY 229 LSGVTLTDTETVYLMDCMSFDTTISTVDTKLSPPCDFLFTDHEWYNYDYLQSLKKYXGHG 288
Db 245 ---LKFTKQDISLWFLCKQVALL-----EWTD-----DLEVFLLKG 278
QY 289 AGNPLGTQGVGYNELIARLTHSPVHDDT--SSNHTLSSPATFLNLTLYA--DFSHD 344
Db 279 YGNSLNYKMGV-----PILEDVLSHMEEAIKAREEKLPPGSEKARLRFABA 325
QY 345 NGIISILFALGLY-NGT-----KELSTTTVENITQTDGSSAWTVPPASRLYVENMQ 395
Db 326 ETIVPFFSCLLGLFDGSEFEKIOKEKLELP--PQPKTRDFRGSTWAPFGNNILVLYS 383
QY 396 COAQEQEP--LVRVLRVNDVRVPLHGCVPDALGRCTRDSF 431
Db 384 CPAESSKYFQVVLNHEHPITAVFGC--DGKDFCFLEDF 419

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Job time : 52 secs